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WPI; 2002-171805/22.	Giver LJ, Minshull J, Vogel K;		(MAXY-) MAXYGEN INC.		21-JUN-2001; 2001US-300378P.	13-JUL-2000; 2000US-217954P.		13-JUL-2001; 2001WO-US22160.		24 - JAN - 2002.		WO200206457-A2.		Bacillus pumilus.		gastrointestinal.	gastrointestinal lipid related condition; antiinflammatory; respiratory	coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;	leather processing; cleaning agent; Crohn's disease; cystic fibrosis;	<pre>human foodstuff; cheese; food emulsifier; leather tanning; enzyme;</pre>	Lipase; Bacillus; animal feed; flavour modification; fat modification;	

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RESULT 2
AAU83847
ID AAU8
XX AAU8
AC AAU8
XX AAU8
AC AAU8
CE Baci
XX Lipa
KW Leat
KW Coel
KW Gast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
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21-JUN-2001;
                                                                          13-JUL-2001; 2001WO-US22160
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                                                                                                                                                                           Bacillus firmus
                                                                                                                                                                                                           gastrointestinal
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2001US-300378P.
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                                                                                                                     human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
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                                            WO200206457-A2
                                                                         Bacillus badius
                                                                                                      gastrointestinal
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209; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acids encoding lipase enzymes which are useful as supplemental feeds, as agents of flavour modification and for treating disease and coeliac disease -
                                                                                                                                                                                     Bacillus;
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RESULT 4
AAU83844
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XX AAU8
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DT 08-h
DT 08-h
DT Bac:
XX Bac:
XX Coel
KW Lipa
KW Loel
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XX Gas
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Sac:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell with an effective amount of DNA or protein of the invention. Sequences AAU03841-AAU083897 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crohn's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-2000;
21-JUN-2001;
                                                                                                                                              Bacillus lipase polypeptide #4.
                                                                                                                                                                                08-MAY-2002
                                                                                                                                                                                                                                              AAU83844 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention. Seque polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding lipase enzymes which are useful as supplements in animal feeds, as agents of flavour modification and for treating Crohn's disease and coeliac disease -
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                                     leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory: resniratory gastrointestinal
                                                                                                                                                                                                                 AAU83844;
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                                                                                                                                                                                                                                                                                                                               QIHGVGHIGLLMNSQVNSLIKEGLNGGGHNTN 212
                                                                                                                                                                                                                                                                                                                                                  QIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN 212
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                                                                                                                Bacillus;
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2001US-300378P.
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                                                                                           animal feed; flavour modification; fat mo
cheese; food emulsifier; leather tanning;
                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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98.1%;
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Pred. No. 5
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                                                                                                            fat modification;
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Bacillus lentus

cystic fibrosis;

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RESULT 5
AAU83845
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Best Local
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                                                Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
                                                                                                                                                                                                            Bacillus lipase polypeptide #5.
                                                                                                                                                                                                                                                                                                                        08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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human foodstuff; cheese; food emulsifier; leather tanning;
leather processing; cleaning agent; Crohn's disease; cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU83845 standard;
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2001US-300378P
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98.1%;
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Pred. No. 9
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gastrointestinal
gastrointestinal
                08-MAY-2002
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21-JUN-2001;
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                                              AAU83846
                                                                          AAU83846 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                    LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
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                (first entry)
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2001US-300378P.
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lipid related condition; antiinflammatory; respiratory;
                                                                          Protein;
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Pred. No. 1.2e-100;
1; Mismatches 4;
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gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                                                                                                     The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other
                                                                                                                                                                                                                                                                                                              Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
Sequence
                                                                                                                                                                                                                                                                               Claim 20; Page 139; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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21-JUN-2001;
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                                polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                     ABK33824.
 212
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2001US-300378P.
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Query Match Best Local :

Local

Similarity

96.2%; 96.7%;

Score 1047; DB 23 Pred. No. 2.6e-99;

DB 23;

Length

212;

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Matches
           1 MKFVKRRIIALVTILVLSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQ
MKFVKRRIIALVTILVLSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQ
                                               205;
                                               Conservative
                                               Ψ
                                               Mismatches
                                               4;
                                               Indels
                                               0;
                                              Gaps
60
                       60
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61 61 GWSRGELYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN 120

121 LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180

LDGGNKIENVVTLGGANRLTTSKALPGTDPNQKILYTSIYSSANMIVMNYLSKLDGAKNV

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Qy В Qγ B Ωy 밁 Qγ

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AAU83849

AAU83849 standard; Protein; 212 A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human foodstuff: cheese; food emulsifier: leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                   Sequence
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                               polypeptides of the invention.
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                                                                                                                                                                                            1 MKFVKRRIIALVTILVLSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQ
                                                                                                                QIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
                          QIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN 212
                                                                      LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                         LDGGNKVENVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLDGARNV
                                                                                                                                                                            MKFVKRRIIALVTILMLSVTSLFALQPSAKAAEHNPVVMVHGIGGASFNFAGIKSYLVSQ
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                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                   212 AA;
                                                                                                                                                                                                                                         Conservative
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2001US-300378P
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Pred. No. 2
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RESULT 8
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ADU 8A942
AC AAU8
XX AAU8
XX AAU8
XX AAU8
XX Lipa
KW Lipa
KW Lipa
KW Costl
KW Gostl
KW Gostl
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XX Baci
XX WO2C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                        GWSRDKLYAVDFWDKTGTNYNNGPVLPRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 138; 196pp; English.
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2001US-300378P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
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                                                                                                                                                                                                                                                                                                                                               92.6%;
92.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vogel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           feed;
                                                                                                                                                                                                                                                                                                                    8;
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                                                                                                                                                                                                                                                                                                                                               Score 1007;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           χ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flavour modification; fat modification;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                               DB 23;
                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as supplements
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AAU83843
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                                                           Ωy
                                                                                                                                                 QΥ
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                                                                                                                    Query Match
                                                                                          Matches
                                                                                                         Best
                                                                                                                                                                                 The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohm's disease, Cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human foodstuff; cheese; food emilsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 138; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-171805/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giver LJ, Minshull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUL-2000; 2000US-217954P.
21-JUN-2001; 2001US-300378P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUL-2001; 2001WO-US22160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipase; Bacillus human foodstuff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2002
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                                                                                                                                                                           polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK33821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus megaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAXY-) MAXYGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 QIHGYGHIGLLMNSQVNSLIKEGLNGGGQNTN 212
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                                                                                                      Local
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                                 QIHGVGHIGLLYSSQVNSLIKEGLNGGGLNTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus; animal feed;
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lipase
                                                                                                                                                212 AA;
                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide #3
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                                                                                                       92.5%;
93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vogel
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                                                                                            Ψ
                                                                                                      Score 1006; DB 23
Pred. No. 4.2e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     condition; antiinflammatory; respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         flavour modification; fat modification;
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                                                                                            Mismatches
                                                                                                                    DB 23;
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                                                                                          Indels
                                                                                                                    212;
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                                                                                       Gaps
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61

GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN 120

Query Match
Best Local Similarity
Matches 196; Conserv

92.5%; 92.5%;

Score 1006; DB 23 Pred. No. 4.2e-95;

Length Indels

212; 0

Gaps

0

6,

Mismatches

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RESULT 10
AAU83855
В
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                                                                                                                                               The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a mathed of badrolusing a limid corporation are attract for lipid mathed by the food of the complete 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                         method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 32; Page 140; 196pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gastrointestinal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus lipase polypeptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU83855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU83855 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
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212
                                                     of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-217954P
2001US-300378P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US22160
                                                     invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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RESULT 11
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                                                                      acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAXY-) MAXYGEN INC
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21-JUN-2001;
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                                                          polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200206457-A2.
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2001US-300378P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 212
                                                             invention.
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                                                                                                                                                                                                                                                                                                                                                                                               new Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                               enzymes
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RESULT 1:
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Best Local S
                                                                                                                                                                                                                                                           WPI; 200
N-PSDB;
       The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a matched of standard treatment or prophylactically treated via a matched of standard treatment.
                                                                                                                                                                                           Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human foodstuff; cheese; food emulsifier; leather tanning; enzyme; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory
                                                                                                                                                             Claim 30; Page 140; 196pp; English.
                                                                                                                                                                                                                                                                                                       Giver
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                    (MAXY-) MAXYGEN INC
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DB; ABK33832.
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2001US-300378P.
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No. 1.2e-93;
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the invention. Se
       The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplement animal feeds, as agents of flavour modification and fat modification human foodstuffs (e.g. cheese), as agents in the creation of food emulations.
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                                                                                                                                                                             Giver
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                                                                                                                      Nucleic
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                                                                                                                                                                                                                                                                                                                                 Synthetic
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                                                                                                                                                                              ĽJ,
                                                                        5:
                                                                                                      acids encoding lipase enzymes al feeds, as agents of flavour
                                                                                            disease and coeliac disease -
                                                                                                                                            ABK33872.
                                                                                                                                                                                                      MAXYGEN
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                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a target cell with an effective amount of DNA or protein ion. Sequences AAU83841-AAU83897 represent Bacillus lipase
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  as agents
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 tanning/processing
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 as agents in the creation of ing/processing of leather and
                                                                                                         which are use
modification
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                                                           Claim
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21-JUN-2001;
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                                                                                             cleic acids encoding lipase enzymes animal feeds, as agents of flavour
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177; Conser
                                                                                   al feeds, as
disease and
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                                                                                                                                                                                                 MAXYGEN INC
                                                                                                                                       ABK33868
                                                           Page 145;
                                                                                                                                                                          Minshull
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2001US-300378P.
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                                                                                    coeliac disease
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98.3%;
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Pred. No. 7e-87;
1; Mismatches
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                                                                                               which are useful modification and
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase polypeptides of the invention.
The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in
                                                                                     Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                            Claim 5;
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21-JUN-2001; 2001US-300378P
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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                                                       Page 144; 196pp; English.
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Pred. No. 1.8e-86;
2; Mismatches 2;
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                                                                                       153 KILYTSIYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKEGLNGGGQNTN
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3, Appli
3301, Ap
4054, Ap
                                                35, Appl
4, Appli
5592, Ap
6, Appli
8, Appli
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2, Appli
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3517, Ap
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Sequence 34, Appl	US-09-268-347-34	4	1104	7.2	78	45
28,	US-09-268-347-28	4	1104	7.2	78	44
Sequence 64, Appl	US-09-562-737-64	4	503	7.2	78	43
Sequence 10, Appl	US-09-165-922A-10	4	371	7.2	78	42
INFORMATION FOR	US/08/622	ω	371	7.2	78	41
Sequence 4412, Ap	US-09-134-001C-4412	4	366	7.2	78	40
Sequence 4056, Ap	US-09-134-001C-4056	4	340	7.2	78	39
Sequence 43, Appl	US-09-136-574A-43	4	1426	7.2	78.5	38
11,	US-09-370-700-11	4	539	7.4	80	37
	US-09-036-987A-11	4	539	7.4	80	36
	US-07-828-980A-2	Н	316	7.4	80	35
Sequence 2927, Ap	US-09-134-001C-2927	4	284	7.4	80.5	34
	US-09-206-942-47	4	1079	7.4	81	33
Sequence 49, Appl	US-09-206-942-49	4	1073	7.4	81	32
Sequence 3465, Ap	US-09-134-001C-3465	4	312	7.4	81	31
Sequence 348, App	US-09-615-192A-348	4	551	7.5	81.5	30
	5472855-5	6	275	7.5	81.5	29
Sequence 13, Appl	US-08-737-716-13	N	671	7.5	82	28

ALIGNMENTS

RESULT 1 US-07-930-678-2

Sequence 2 Patent No.

, Application 5427936

US/07930678

INFORMATION:

MOELLER,

Bernhard

APPLICANT:
APPLICANT:
APPLICANT:

VETTER, Roman WILKE, Detlef FOULLOIS, Birgit

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JS-07-930-678-2
                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/EI
FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: F10ppy disk
COMPUTER: IBM PC COMPATIBLE
COMPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Alkaline Bacillus Lipases,
TITLE OF INVENTION: Sequences Therefor and Baciltus Of INVENTION: Lipases
                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                  SEQUENCE CHARACTERISTICS:
                             TYPE: AMI
                                                                                                                                                                                                       REGISTRATION NUMBER: 26,269
                                                                                                                                                                                                                               NAME:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USE FILING DATE: 19921013
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ZIP: 22313-0299
                                                                   LENGTH:
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1800 Diagonal Road,
                                                                 213 amino acids
                                                                                                                                       (703)683-4109
                                  linear
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              protein
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14-APR-1990
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Therefor and Bacilli, Whicch Produce These
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Best Local Similarity 73.9
Matches 156; Conservative
              Query Match
Best Local Similarity
 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10,
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                                                                                                                                        NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                    TOPOLOGY: 11
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acid
                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 WSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNL 121
                                                                                                                                                                  TELEFAX:
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                                                                                                                                                                                                                          NAME: Kokulis, Paul N
REGISTRATION NUMBER:
                                                                                                                                                                                                                                        NAME:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/727,235 FILING DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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6714627 CUSH
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                                                                                                           358 amino acids
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           12.8%;
29.6%;
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73.9%;
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 26;
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Pred. No. 3.7e-79;
                                                                                                                                                                                                             PNK/5970/91731
              Score 139.5; DB 1; Pred. No. 5.6e-07;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                Version #1.25
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 Indels
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 29;
Gaps
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US-08-449-015-10
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Best Local Similarity 29.6%; Pred. No. 5.6e-07.
Matches 48; Conservative 26; Mismatches 59
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                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Kokulis, Paul N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 03-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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CITY: Washington
                                                                                  49
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/449,015 FILING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20036-5601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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  99 AKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRST 140
                                         61 KFANYVDYWYGIQSDLQSHG----AKVYVANLSGFQSDDGPN-GRGEQLLAYVKQVLAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kokulis, Paul N
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KFANVVDYWYGIQSDLQSHG---AKVYVANLSGFQSDDGPN-GRGEQLLAYVKQVLAATG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 NFA-----GIKSYLVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETG
                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                           N
                                                                                                                                                                1 MKFVKRRIIALVTILVLSVTSL-----FAMQPSAKAAE-----HNPVVMVHGIGGASY 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKFVKRRIIALVTILVLSVTSL-----FAMQPSAKAAE-----HNPVVMVHGIGGASY
                                                                                NFA-----GIKSYLVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETG 98
                                                                                                                         VRSMRSRVAARAVAWALAVMPLAGAAGLTMAASPAAVAADTYAATRYPVILVHGLAGTD- 60
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VERRIPS, Cornelis T.
VISSER, Christiaan
VISSER, Christiaan
VERNTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUMAE
TIPASE IN HOMOLOGOUS OR HETEROLOGOUS HO
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FRENKEN, Leon G
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                        Sequence 1, Application US/09336601 Patent No. 6184008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                        GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08978589A Patent No. 6087145
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
         APPLICANT: ISHII, Takeshi
APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
                                                                APPLICANT: OHTA, Hiromichi
APPLICANT: SUGAI, Takeshi
APPLICANT: ISHII, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 205-80:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ISHII, APPLICANT: MITSUDA, SATOSHI
APPLICANT: MYENTION: ESTERASE GENE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                138
                                                                                                                                                                                                                                                                               116 YYIKNLDGGNKIENVVTLG----GANRSTTSKALPGTDP 150
                                                                                                                                                                                                                                                                                                                  80 DLRAHGAAVYVANLSGFQSDDGPN-GRGEQLLAFVKQVLAATGAQKVNLIGHSQGGL-TS 137
                                                                                                                                                                                                                                                                                                                                                       65
                                                                                                                                                                                                                                                                                                                                                                                                                          13 TILVLSVTSLFAMQPSAK-----AAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         26 TVLAMSLAGAQAASAATTAVDDYAATRYPIILVHGLTGTD-KYGGVVEY-----WYRIPE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                      -----GKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTP 115
                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                              RYVASV-APELVASVTTISTPHWGSQFADFVQQLLQTDP 175
APPLICATION NUMBER: US/09/336,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: BIRCH, STEWART, T: P.O. BOX 747 FALLS CHURCH: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 amino acids
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SYSTEM: PC-DOS/MS-DOS
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205-8050
207 NO: 2:
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Pred. No. 3.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                    REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
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                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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10174-6201
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212 867 0298
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18-DEC-1992
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SEQ ID NO 3301
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3301, Application US/09134001C Patent NO. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AUTITLE OF INVENTION: EPIDERWIDIS FOR D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: 1 ORIGINAL SOURCE:
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   196 KQGKPSRMNAAYRQLLSLYKIYCGKEIEVLNIYGDLEDGSHSD-----
                                                             143 KALPGTDPN----QKILYTSIYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSQVNS 198
                                                                                                                                   136 FGIQQFNFVGHSMGNISFAFYMKNYGDDRHLPQLKKEVNIAGVYNGILNMNENVNEIIVD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                           97 TGAKKVDIVAHSMGGANTPYYIKNLDGGN---KIENVVTLGG----
                                                                                                                                                                                                                                                                                76 VTNEVITARVSSEGKVYFDKKLSEDAANPIVKVEFKDNKTGNFKENAYWIKEVLSQLKSQ 135
                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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19.9%; Pred. No. 0.016;
tive 38; Mismatches 90;
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Pred. No. 0.00035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 292;
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                                                                                                                                                                                                        ----ANRSTTS 142
-GRVSNSSSQS 248
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; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4568
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US-09-134-001C-4054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4568
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LENGTH: 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
  Best Local Similarity
Matches 54; Conserv
                                         Query Match
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS EILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
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                                                                                                                                       LENGTH: 690
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSMGGQT----IRQLEELLRHGNPEEVEYQKQHGGEISPLFQGGHDNMVSSITTLGTPHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
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                   8.4%; Score 91.5; DB 20.4%; Pred. No. 0.26;
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    Mismatches
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                                            DB 4;
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                                              Length 690;
  Indels 107;
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                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                          MOLECULE TYPE:
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 YDRAVELYYYVKGGRVDYGAAHAAKYGHHRYGRTYKGIMRDWEPGKKIHFIGHSMGGQTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 PVVFVHGFLGFAGDNQFSLAPKYWGGTKYN---IDRNLTNEGYNVHEANIGAF----SSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Virginia
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                                             Local
                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                               NAME: Oblon, No. 5306633man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                            FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                 CELEPHONE:
 2 KFVKRRIIALVTILVLSVTSLFAMQPSAKAAEH------NPVVMVHGIGG-ASYNFAG
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                                                                                                                                                                                                                 : (703) 413-3000
(703) 413-2220
                                Conservative
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                                         8.1%;
25.2%;
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                                           Pred. No.
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                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: EP 9
FILING DATE: 04-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM
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118
                                                                                                                                    13 TILVLSVTSLFAMQPSAKAA-----EHNPVVMVHG-----IGGASYNFAGIKSYL
                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                             65 RSDGAS---VYITEV-SQLNTSELRGEELLEQVEEIAAISGKGKVNLVGHSHGGPTVRYV 120
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                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                                                                                       CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE:
                                                                        VSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TGAKKVDIVAHSMGG-----ANTPYYIKNLDGGN 125
                                                                                                       TLLALCIGSSLLLSGPAEAGLFGSTGYTKTKYPIVLTHGLLGFDSILGVDY-WYGIPSSL
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                                                                                                                                                                 l Similarity
52; Conserv
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Gerritse, Gijsbert
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                                                                                                                                                                              Score 87.5; DB Pred. No. 0.21;
                                                                                                                                                                 Mismatches
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                                                                                                                                                                                              DB 3;
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                                                                                                                                                                                              Length 313;
                                                                                                                                                                 Indels
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RESULT 13
US-08-456-956-2
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US-08-232-519-2
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Sequence 2, Application US/08456956 Patent No. 5686285
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REFERENCE/DOCKET NUMBER: SHGN-4
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nakae, Masanori
                                                                                                       248 AFVDSESSRDM-----KAVLQMLVYNKALVGRKMVDAVLR--ARRLDGARDA
                                                                                                                                                                           188
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TELEFAX: 14-8367
                                                                                                                                       135 GANRSTTSKALPGTDPNQKILYTSIYSSA-----DMIVMNYLSKLDGAKNA 180
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                                                                                                                                                                                                                                           134 EGTPIVLVHGEGG-----DISNWLLTQDALAAERRVIAFDLPGHGASSKNVGTGTLAFL 187
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                                                                                                                                                                                                        87 SREVQKVLDETGAKKVDIVAHSMGGA-----NTPYYIKNLD-----GGNKIENVVTLG 134
                                                                                                                                                                                                                                                                             33 EHNPVVMVHGIGGASYNFAGIKSYLVSQG--WSRGKLYAVDFWDKTGTNYNNG----PVL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION:
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les 40; Conserv
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                                                                                                                                                                        AGVVSELLQTLKIEKAHVVGHSLGGGIALTLLRDHPDQVASLNLLAPAGLGKDVNADFIS
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23.1%;
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US-09-134-001C-3517
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                                                                                                                              GENERAL INFORMATION:
                                                                                                                                             Sequence 3517, App
Patent No. 6380370
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
                                                                      APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: EPIDERMIDIS FOR
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
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APPLICATION NUMBER:
FILING DATE: 22-APR-
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TELEPHONE: (212)596-9090
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Local Similarity 23.1%;
nes 40; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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ZIP: 10020
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                                                                                                                                                                Application US/09134001C
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Pred. No. 0.3;
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                                                                        AMINO ACID SEQUENCES RELATING DIAGNOSTICS AND THERAPEUTICS
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SEQ ID NO 3517

PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US: 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

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; LENGTH: 652
; TYPB: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-111-556A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                     TELEPHONE: 212-867-0123
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK PCT/DK93/00225
FILING DATE: 03-JUN-1993
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Clausen, Ib G
APPLICANT: Hansen, Mogens T
ITILE OF INVENTION: C. ANTAH
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                433 GT----PAAD---KLGSTKFIKD----TINRIGKIGGTK 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 HLVGHSMGGQTIRLMEHFLRNGNQEEIDYQRQYGGTVSDLFKGGQDNMVSTITTLGTPHN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 QLTAQAQYKNQYPVVFVHGFVGLVGEDAFSMYPNYWGGTKYN---VKQELTKLGYRVHEA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 DIVAHSMGGAN---TPYYIKN-----
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                                                                                          NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 22-DE
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: United States of America ZIP: 10174-6401
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                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                         CLASSIFICATION:
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Egel-Mitani, Michi
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                                                                                                                                                                                                                                          22-DEC-1994
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mgr: 3748.214-US
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                     <u>ω</u>
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Pred. No. 0.74;
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-111-556A-3
Search completed: May
Job time : 16 secs
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                                                                                                                                                                                                     Query Match 8.0%;
Best Local Similarity 26.4%;
Matches 29; Conservative 21
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                                                                                                    91 OKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRST 140
                                                                                                                                      10 PILLVHGLFGFDRIGSHHYFHGIKQALNECGAS----VFVPIISAANDNEARGDQLLKQI 65
                                                                                                                                                                      36 PVVMVHGIG-----GASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFV
                                                                    HNLRRQVGAQRVNLIGHSQ-GALTARYVAAI-APELIASVTSVSGPNHGS 113
                 9, 2003, 16:22:45
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Pred. No. 0.23;
1; Mismatches
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
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Gapop 10.0 , Gapext 0.5
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9 US-10-147-467-2
12 US-10-080-644-6
10 US-9-815-242-5111
12 US-10-080-644-8
11 US-10-080-644-8
11 US-10-080-644-2-1186
10 US-9-815-242-2181
10 US-09-8174-1
12 US-10-080-644-2
11 US-10-080-644-2
12 US-09-815-242-5841
19 US-10-027-805-35
10 US-09-804-35
10 US-09-813-408-35
10 US-09-3-410-35
10 US-09-3-816-55
10 US-09-738-656-5
10 US-09-813-408-15
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US-09-738-626-3594
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                                            Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 11886, A
Sequence 281, Appli
Sequence 2, Appli
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 35, Appl
                                                                                                                                                                                                                                                              Sequence 4, Appli
Sequence 3593, Ap
Sequence 3594, Ap
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                         Description
                                 Sequence 5, Appli
Sequence 3604, Ap
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45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23		21	20
74	74.5	74.5	74.5	74.5	74.5	75	75	75	75.5	. 76	76	76	76	76	76	76	76.5	76.5	77.5	77.5	78	79	79	79	79
٠						6.9		6.9		7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.0	7.1	7.1	7.2	7.3	7.3	7.3	7.3
184	363	274	274	274	274	1781	535	297	380	434	357	280	275	275	275	275	372	254	1093	495	503	1463	871	836	235
10	9	10	9	9	<u>-</u>	9	9	12	9	9	10	10	10	9	φ	_	9	12	10	9	9	9	9	9	9
US-09-734-017A-78	US-09-797-464A-11	US-09-060-854B-5	US-10-033-325-5	US-09-813-408-17	US-08-322-678-9	US-09-995-749A-2	US-09-995-749A-13	US-10-080-644-7	US-09-813-408-16	US-09-971-536-62	US-09-837-235-15	US-09-731-872-314	US-09-060-854B-4	US-10-033-325-4	US-09-813-408-18	US-08-322-678-8	US-09-813-408-9	US-10-080-644-5	US-09-801-368-392	US-10-213-990-42	US-10-211-962-64	US-09-971-536-69	US-09-858-525A-2	US-09-858-525A-10	US-09-533-029-74
e 78,	11,	е 5	5, A	Sequence 17, Appl	Sequence 9, Appli	Sequence 2, Appli	13,	e 7,	16,	52, A		314	e 4,	4, 1	18,	Sequence 8, Appli	Sequence 9, Appli	Sequence 5, Appli	Œ	42,	64,	69,	2, A	10,	Sequence 74, Appl

ALIGNMENTS

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                                                                                                                                                                                                                                    Query Match 97.4%;
Best Local Similarity 97.6%;
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10028247 Patent No. US20020150594A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Maxygen, Inc.

TITLE OF INVENTION: Methods and Compositions for Developing Spore Display

TITLE OF INVENTION: Systems for Medicinal and Industrial Applications

FILE REFERENCE: 18097A-033520US

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: US 60/214,161

PRIOR APPLICATION NUMBER: US 60/214,161

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: US 09/892,208

PRIOR APPLICATION NUMBER: US 09/892,208

PRIOR FILING DATE: 2001-06-26

PRIOR FILING DATE: 2001-06-26

RUMBER OF SED ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Goldman, Stanley APPLICANT: Lathrop, Stepha
                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Bacillus circulans
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 212
121 LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                         GWSRGKLYAVDEWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN 120
                                          GWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN
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Longchamp, Pascal F.
Whalen, Robert G.
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                Score 1060; DB 12
Pred. No. 6.9e-97;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                        DB 12;
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                                                                                                                                                                                                                                                                                                              RESULT 3
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US-09-738-626-3593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 35; Conserv
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SEQ ID NO 3593
LENGTH: 324
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                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                                                            Sequence 3594, Application US/09738626 Publication No. US20020197605A1
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                       APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
                                     FILE REFERENCE:
                                                                                                                        APPLICANT:
                                                                                                                                        APPLICANT:
                                                                                                                                                                       APPLICANT:
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                                     TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                               148 LATGASKVIVVGHSQGGVLLRYWMRVLGGASKVKHMVSLAVPNHGTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                               91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDK-TGTNYNNGPVLSRFVQKVL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN 212
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                                                                                                                                                                                                                                                                                                                                                                                                                               PVVLVHGTGSTKGDWQDLGADLRRDGWA---VFAPEFGQRATGSVAESSAQIGAYIDTVL 147
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IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                    OCHIAI, KEIKO
YOKOI, HARUHIKO
                                                                    IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                                                    HAYASHI, MIKIRO
                                                                                                 TATEISHI, NAOKO
SENOH, AKIHIRO
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Pred. No. 1.9e-07;
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APPLICANT: Glucksmann, Maria, Alexandra
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 3594
LEEGTH: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Burkholderia cepacia US-10-147-467-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-10-147-467-2
                                                                       US-10-080-644-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10147467
Publication No. US20030027295A1
GEMERAL INFORMATION:
APPLICANT: TAKESHI, Ishii
APPLICANT: SATOSHI, Mitsuda
TITLE OF INVENTION: ESTERASE GENE AND
FILE REFERENCE: 20-4336P
Sequence 6, Application US/10080644 Patent No. US20020137172A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 363
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 2002-05-17
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                                                                                                                                                                      138 RYVASV-APELVASVTTISTPHWGSQFADFVQQLLQTDP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 SKALPGTDPNQKILY 156
                                                                                                                                                                                                                     116 YYIKNLDGGNKIENVVTLG----GANRSTTSKALPGTDP 150
                                                                                                                                                                                                                                                                                                                                                                                         13 TILVLSVTSLFAMQPSAK-----AAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR--- 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 IDAVLLVTGAAQIVLVGHSQGGVVARYWMRTYGGYMKVRHMISISTPNHGTLMGGILNPM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPV-----LSRF 89
                                                                                                                                                                                                                                                                                                                                                                26 TVLAMSLAGAQAASAATTAVDDYAATRYPIILVHGLTGTD-KYGGVVEY-----WYRIPE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 VQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRST-----T 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 PIVLIHGSGASKGSWEEMGAELRSKGWA---VFAPDF----GTRATE-PIAASAAQIGAY 123
                                                                                                                                                                                                                                                              DLRAHGAAVYVANLSGFQSDDGPN, GRGEQLLAFVKQVLAATGAQKVNLIGHSQGGL-TS 137
                                                                                                                                                                                                                                                                                                               -----GKLYAVD----FWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTP 115
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TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-080-644-6
                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa US-09-815-242-5111
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 299
                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/584,568 PRIOR FILING DATE: 2000-05-31
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CURRENT FILING DATE: 2002-02-22
                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                                                                                              TYPE: PRT
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                3 FVKRRIIALV---TILVLSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKS----
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                                                                                                                                                                                              NO 511
                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                  FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/242,578
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                                                                                                                                                                                                                                                                                                                                                   ILING DATE: 2000-10-23
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o. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
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Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert T.
                                                      Conservative
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                                                                                                                                                                                                                                               2001-02-16
                                                                      8.5%;
25.3%;
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27.6%; Pred. No. 0.0
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                                                  Score 92.5; DE
Pred. No. 1.8;
22; Mismatches
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US-09-815-242-11886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11886, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10080644 Patent No. US20020137172A1
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                                                                                                   TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERNCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/584,568
PRIOR FILING DATE: 2000-05-31
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TITLE OF INVENTION: 33167, A NOVEL HUMAN-HYDROLASE
                                                              PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
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TYPE: PRT
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                      PRIOR
                                       PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 PDNRYDMLYLSNY--AVLNVKDELARLDGVGDVQLFGLGDYSLRVWLDPNKVASRNL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 VLDETGAKKVDIVAHSMGGANTPYYIK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
APPLICATION NUMBER: 60/242,578
                      FILING DATE: 2000-05-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLLTYHGLFGSKQNWRGISKALVRK-VSR-KVYAIDVRNHGESPHSSVHNSKAMSEDLRL 111
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                                                                                                                                                                                                                                                                            Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                              Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
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Pred. No. 0
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PRIOR FILING DATE: 2000-10-23

APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27

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Best Local Similarity
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                                                                                                                                                                                                                                                                                              ; TYPE: PRT ; ORGANISM: E. Coli US-09-912-020-281
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US-09-815-242-11886
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PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
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PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                      LENGTH: 464
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                                  158 SIYSSADMIVMNYLSKL-DGAK 178
415 AGISAGDRVVTDGIDRLTEGAK 436
                                                                                                             116
                                                                                                                                           297 VVQAQKAGKPLVVEAWDRTNSKKLSEGTLLS--LDNQIDATTGTIKVKARFNNQDDALFP 354
                                                                                                                                                                               58 VSQGWSRGKLYAVDFWDKTGT-NYNNGPVLSRFVQKVLD-ETGAKKVDIVAHSMGGANTP 115
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                                                                      NQFVNARMLVDTEQNAVVIPTAALQMGNEGHFVWVLNSENKVSKHLVTPGIQDSQKVVIR 414
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Forsyth, R. Allyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu, H. Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Froelich, Jamie M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T
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20020045592A1
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25.4%;
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Pred. No. 1.
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Pred. No. 0.93;
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US-10-080-644-2
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US-10-098-174-1
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US-10-098-174-1
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LENGTH: 518
TYPE: PRT
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Best Local Similarity 21.4
Matches 47; Conservative
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                                                                                                                      Matches
                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                     SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10080644 Patent No. US20020137172A1
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/584,568 PRIOR FILING DATE: 2000-05-31
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APPLICANT: BOWDEN, Maria
TITLE OF INVENTION: COLLAGEN-BINDING ADHESIN FROM STAPHYLOCOCCUS EPIDERMIDIS.
FILE REFERENCE: P07136US01/BAS
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/080,644
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Glucksmann, Maria, Alexandra et al.
TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR
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CURRENT FILING DATE: 2002-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: MNI-140
                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            LENGTH: 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 STTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAK 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 NVGAF----SSNYDRAVELYYYIKGGRVDYGAAHAAXYGHKRYGRTYEGIMPDWEPGKKI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 GT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 HLVGHSMGGQTIRLMEHFLRNGNQEEIDYQRQYGGTVSDLFKGGQDNMVSTITTLGTPHN 266
                                                                                                                                            Local Similarity
                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94 QLTAQAQYKNQYPVVFVHGFVGLVGEDAFSMYPNYWGGTKYN---VKQELTKLGYRVHEA 150
  89 FVQKVLDETGAKKVDIVAHSMGG 111
                                                                              37 VVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGP------VLSR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 YAVDFWDKTGTNYNNGPVLSRFVQKVLDETGA------
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                                        VVFLHGLFGSKTNFNSIAKILAQQTGRR--VLTVD--
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                                                                                                                      Conservative
                                                                                                                                         8.0%;
30.1%;
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21.4%; Pred. No.
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Pred No. 1.3;
                                                                                                                    Mismatches
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                                    -ARNHGDSPHSPDMSYEIMSQ 121
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US-10-027-805-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-815-242-5841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ
SEQ ID NO 5841
LENGTH: 690
                                                               Sequence 35, Application US/10027805 Patent No. US20020164725A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Haselbeck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION NUMBER: 60/191,078 RIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: Prokaryotes ILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Identification of Essential Genes in ITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IOR APPLICATION NUMBER: 60/206,848 IOR FILING DATE: 2000-05-23
                                                                                                                                                                                          4.82 KIMFALNRFMGNKYSNIDL 500
                                                                                                                                                                                                                                                                                                                                                                                                                 306 PVVFVHGFLGLVGDNAPALYPNYWGGNKFKVIEELRKQGYNVHQASVSAF----GSNYDR 361
                                                                                                                                                                                                               153 KILYT-----SIYSSADM 165
                                                                                                                                                                                                                                                                   422 EEFLRNGNKEEIAYHKAHGGEISPLFTGGHNNMVASITTLATPHNGSQAADKFGNTEAVR
                                                                                                                                                                                                                                                                                                       118 IKNLDGGNKIE------NVVTLGGANR---STTSKALP----
                                                                                                                                                                                                                                                                                                                                          362 AVELYYYIKGGRVDYGAAHAAKYGHERYGKTYKGIMPNWEPGKKVHLVGHSMGGQTIRLM 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 DLQDLLPQLGLVPCVVVGHSMGG 144
                                                                                                                                                                                                                                                                                                                                                                              83 GPVLSRFVQKVLDETGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 PVVMVHGIGG------ASY-NFAGIKSYLV-----SQGWSRGKLYAVDFWDKTGTNYNN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                              APPLICANT: ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5841, Application US/09815242
o. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/815,242 FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen, Kari L.
Zyskind, Judith W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trawick, John D.
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MURPHY, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-02-16
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                          Dennis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 86.5; DF Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                            ---KKVDIVAHSMGGANTPYY 117
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US-10-027-804-35
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                                                                                                                                                                       Sequence 35, Application US/100. Publication No. US20030054530A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     128 LHRI--GYPLAKILASIAYKKSSRLV----ADLSFGKNA 160
                                                                                                                                                                                                                                                                                                                                        142 SKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            70 RFENFISDLDAVVRETGVEKFVLVGHSFGTMISMKYCS--EYRNRVLALILIGGGSRIKL 127
                                                                                                                                                                                                                                                                                                                                                                                                             88 RF-----VQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 PIVFVHG-WTANMNF------WKEQRRYFAGRNMMLFVDNRGHGRSDKPLGYDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD----FWDKTGTNYNNGPV---LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ESTERASES
           TITLE OF
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TELEPHONE: 619-678-5070
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                                                                                                                                                     APPLICANT: ROBERTSON, Daniel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 262 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/027,805 FILING DATE: 21-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/602,359 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: LA JOLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: HAILE, LISA A. REGISTRATION NUMBER: 38,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09010/010001
                                                                                                                                                                                                         Application US/10027804
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                                                                                                   ROBL.
MURPHY, L.
TTD, John
An'
                     SWANSON, Ronald V. WARREN, Patrick V. KOSMOTKA, Anna
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                                                                                  LINK,
                                                                                              MAFFIA,
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LINK, Steven
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                                                                          Steven
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                                                                                              Anthony
                                                                                                                                    Dennis
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Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
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87

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NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
CORRESPONDENCE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400

STATE: CALIFORNIA CITY: LA JOLLA

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                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/09903410 Patent No. US20020146799A1
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              CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
                                                                        APPLICANT: KOSMOTKA, ADDA TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOFFILE REFERENCE: DIVER1180-2
PRIOR FILING DATE:
                                                                                                                                                                                                                                                         APPLICANT: DIVERSA CORPORATION APPLICANT: ROBERTSON, Dan
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                                                                                                                                                                                                                                                                                                                                                                                                                                         128 LHRI--GYPLAKILASIAYKKSSRLV----ADLSFGKNA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD-----FWDKTGTNYNNGPV----LS 87
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 619-678-5070
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                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                  LINK, Steven
SWANSON, Ronald
WARREN, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/602,359 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HAILE, LISA A. REGISTRATION NUMBER: 38,347
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TYPE: AMINO ACID
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                                                                                                                                                                                                                   MURPHY, Dennis
REID, John
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25.2%; Pre
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Best Local Similarity
Matches 40; Conserva
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                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 08/602,359 PRIOR FILING DATE: 1996-02-16
                                                                                                                                                                                                                                                                                                                 LENGTH: 262
TYPE: PRT
128 LHRI--GYPLAKILASIAYKKSSRLV----ADLSFGKNA 160
                                  142 SKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNA 180
                                                                                                                                                            36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVD-----FWDKTGTNVNNGPV---LS 87
                                                                     70 RFENFISDLDAVVRETGVEKFVLVGHSFGTMISMKYCS--EYRNRVLALILIGGGGSRIKL 127
                                                                                                    88 RF-----VQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTT 141
                                                                                                                                      22 PIVFVHG-WTANMNF--
                                                                                                                                                                                                                                                                                                                                                                   PatentIn version 3.0
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                            7.8%;
                                                                                                                                                                                                           23;
                                                                                                                                                                                                          Score 85; DB 1
Pred. No. 1.5;
23; Mismatches
                                                                                                                                        -WKEQRRYFAGRNMMLFVDNRGHGRSDKPLGYDFY 69
                                                                                                                                                                                                                                              10;
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Gaps

Search completed: May Job time : 22 secs 9, 2003, 16:29:38

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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2: pir2:*
3: pir3:*
4: pir4:*
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T248953
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GWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKN

Вb

61 61

Query Ma Best Loc Matches	RESULT 1 \$23934 \$23934 C:Species: Bacillus subtilic C:Date: 22-Nov-1993 #sequen C:Accession: \$23934; B69652 R:Dartois, V.; Baulard, A.; Biochim. Biophys. Acta 1131 A;Title: Cloning, nucleotid A;Reference number: \$23934; A;Accession: \$23934 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-212 <dar> A;Cross-references: GB:M740 R:Kunst, F.; Ogasawara, N.; C: Bron, S; Brouillet, S. A; Ehrlich, S.D.; Emmerson Nature 390, 249-256, 1997 A;Authors: Foulger, D.; Fri iech, J; Harwood, C.R.; Hei Koetter, P.; Koningstein, G A;Authors: Lauber, J; Laza y, M.; Ogawa, K.; Ogiwara, Rieger, M.; Rivolta, C.; RR A;Authors: Schleich, S.; Sci akeuchi, M.; Tamakoshi, A.; T; Winters, P.; Wipat, A.; A;Title: The complete genome A;Reference number: 46580; A;Status: preliminary; nucle A;Genetics: A;Geneetics: A;Geneeti</dar>		30 32 33 33 33 33 33 33 34 35 44 44 39 44 39
atch bal Simi 197;	SULT 1 Species: Bacillus subtilis pase lipA - Bacillus subtilis Date: 22-Nov-1993 #sequence Accession: S23934; B69652 Dartois, V.; Baulard, A.; Schim, Biophys. Acta 1131, Title: Cloning, nucleotide Reference number: S23934; MACCESSION: S24000; S24000; S24000; S24000; S24000; S24000; S24000; MACCESSION: B69652 Experimental source: Strain Genetics: GB:Z99105 Gene: lipA		1104.5 1101.5 1001.5 97.5 96.5 96.5 96.5 96.5 97.5 97.5 97.5 98.5 98.5 98.5 98.5 98.5
larity Conservat	us sub/ 93 #see 93 #see 93 #see 93 #see 93 #see 93 #see 10		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
93.8% 92.9% 7ative	subtilis subtilis sequence_ Be9652 cd AA; Sc ca 1131, 2 lleotide s S23934; MU AR BEN74010; AR BE		299 237 299 681 268 1519 1335 377 438 267 268 688 688 688 638
9 as	revis rehanck 253-26 sequen UID:92 UID:92 Franck P.T.; C.; Krogh Fr.T.; Coeter; anamact anamac		000000000000000000
Score 1020; DB 2; 1 Pred. No. 1.8e-77; 8; Mismatches 7;	RESULT 1 S23934 lipA - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Accession: S23934; B69652 C;Accession: S23934; B69652 R;Datrots, V; Baulard, A; Schanck, K; Colson, C. Biochim. Biophys. Acta 1131, 253-260, 1992 A;Hitle: Cloning, nucleotide sequence and expression in Escherichia col. A;Reference number: S23934; MUID:92329538; PMID:1320940 A;Accession: S23934 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-212 CDAR> A;Cross-references: GB:M74010; NID:g143153; PIDN:AAA22574.1; PID:g14315-A;Coss-references: CB:M74010; NID:g143153; PIDN:AAA22574.1; PID:g14315-A;Coss-references: CB:M74010; NID:g143153; PIDN:AAA22574.1; PID:g14315-A;Coss-references: CB:M74010; NID:g143153; PIDN:AAA22574.1; PID:g14315-A;Coss-references: GB:M74010; NID:g143153; PIDN:AAA22574.1; PID:g14315-A;Coss-references: GB:MID:g14315-A;Coss-references: GB:MID:g14315-A;Coss-references: GB:MID:g14315-A;Coss-references: GB:MID:g14315-A;Coss-references: GB:MID:g144-A;Coss-references: GB:MID:g144-A;Coss-r	ALIGNMENTS	AF1193 T26660 T23932 G90075 S41525 541525 T17508 H82713 B83295 F90516 A47705 B47706 B47708 AH0340 S68970 F83335 T30830
Length 212; Indels 0; Gaps 0;	RESULT 1 Lipase lipA - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Accession: S23934, B89652 A;Pitle: Cloning, nucleotide sequence and expression in Escherichia coli of a lipase A;Bactols, V; Baulard, A; Schanck, K; Colson, C. Biochim. Biophys. Actallil; 253-260, 1992 A;Pitle: Cloning, nucleotide sequence and expression in Escherichia coli of a lipase A;Bactols type: DNA A;Bacillus: preliminary A;Molecule type: DNA A;Scatus: preliminary A;Molecule type: DNA A;Cocssion: S23934; MUID:92329538; PMID:1320940 A;Accession: S23934; MUID:92329538; PMID:1320940 A;Scatus: preliminary A;Molecule type: DNA A;Cocssion: S23934; MUID:92329538; PMID:1320940 A;Bacidus: 1-212 cDAR A;Cocssion: S2394 A		hypothetical prote hypothetical prote hypothetical prote triacylglycerol li triacylglycerol li major ring-forming glycoprotein Vp260 triacylglycerol li hypothetical prote esterase/lipase 1 triacylglycerol li periplasmic amino putaive autotransp triacylglycerol li periplasmic amino putaive autotransp triacylglycerol li RND multidrug effl hypothetical prote

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A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scarola, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scarola akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A;Reference number: A69580; MUID:98044033; PMID:9384377

A.;Accession: C69652

A. Statue. The complete genome sequence of the Gram, positive bacterium Bacillus subtilis.
                                                                                                                    C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: G75316
                                                                                                                                                            probable lipase -
C;Species: Deinocc
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                                        M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano,
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A; Residues: 1-210 <KUN>
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C;Species: I
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;Species: Bacillus subtilis
;Date: 05-Dec-1997 #sequence_revision
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    Genome sequence of the radioresistant bacterium nce number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                           DGGNKIENVYTLGGANRSTTSKALPGTDPNQKILYTSIYSSADMIVMNYLSKLDGAKNAQ
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68.2%;
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Pred. No. 1.66
23; Mismatches
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T.; Zalewski,
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                      radiodurans
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A; Residues: 1-290 <SAU>
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A; Residues: 1-237 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCOEDB: SCI11.24c
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 57; Conserv
  protein sll1969
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C; Accession: T36757
R; Saunders, D.; Harris, D.; James, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1 20, 300. A; Cross-references: GB: AE002044; A; Cross-references: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable secreted lipase - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: G75316
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                   23 FAMOPSAKAAEHNPVVMVHGIGGASY-NFAGIKSYLVSQGWSRGKLYAVDFWDKTGTN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKFVKRRIIALVTILVLSVTSLFAMQPSAKAAE-----HNPVVMVHGIGGASYNFAGIK
                                                                                                                                                                                                           YNNGPV-----LSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTL 133
LATKYDEVVTPYRGQFLDG
                                          IYSSADMIVMNYLSK-LDG
                                                                                                                                    GGANRSTT - - - - SKALP - - - -
                                                                                                                                                                                 HGLGPVEKSAEQLAAHVDKVLAATGATETDLVGHSQGGMMPRXYLKFLGGAAEVNALVGI
                                                                                                                                                                                                                                                                          YTCKPS--AAHPRPVVLVHGTFGNSVDNWLGLAPYLKNRGYC---VFSLDYGQLPGVPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RYATWWSPCDAVINPNSSVPLSGATNTKTSCLTHSSLYGDATVYTQVRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LYTSIYSSADMIV-MNYLSKLDGAKNAQIHGVGHIGLLMNSQVNSLIKE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RYYLKNIGGTAKVDAWVSLGGPNHGTDFALACSTASCIEMRQGSSFIKALNSGDETPGAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYYIKNLDGGNKIENVVTLGGANR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRFKQDGWTDAQLFSWSY-DSFKSNAVTADLLRQKVDAILAQTGAAQVDIVSHSMGALSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAFSKRFVLLPLSAALLAGCGTLTQAPSELSAQALAAPVRHPVLFVHGFNSDGSIWSPMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source: strain
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:AL096849; PIDN:CAB50950.1; GSPDB:GN00070; SC0EDB:SC111.24c
                                                                                                                                                                                                                                                                                                                                                                                     16.4%;
28.6%;
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                                            176
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Pred. No. 5.7e-10;
7; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                  Score 178; DB 2;
Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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1999
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 290;
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                                                                                                                                    GTDPNQKILYTS 158
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Synechocystis

sp.

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PCC

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hypothetical protein Y38E10A.g - Caemorhabditis elegans C:Species: Caemorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C:Accession: T26657 R:Wallis, J.
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:AL110484; PIDN:CAB54398.1; CESP:Y38E10A. A;Experimental source: clone Y38E10A C;Genetics: A;Gene: CESP:Y38E10A.9 A;Introns: 63/2; 221/2; 261/3 C;Superfamily: Caenorhabditis elegans hypothetical protein C09E8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Synechocystis sp.
A, Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S77556
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, September 1999 A;Reference number: Z20252 A;Accession: T26657
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A; Residues: 1-286 <W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-202 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Start codon:
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated
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K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.;
IA Res. 3, 109-136, 1996
                                                                                                                                                          126 MIIAVNAFTQQKVNVIGYSMG---SPIARKAILGGKCAENTVQLGAPLTSIIETYISVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
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                                                                                                                                                                                                94 ----LDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLG-----
                                                                                                                                                                                                                                          66 PVILVHGTTNSAGTFAPQAAYFRANGWSEETVYATTYGDAGVTTATNVKMLCEYVQQIRN 125
                                                                                                                                                                                                                                                                                36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKV---
                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 AKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSR
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NTVCGRVSRIDGATAEKDNVPGNHDAIIANT
                                      MIVMNYLSKLDGAKNAQIHGVG-HIGLLMNS
                                                                              ANRGTSLCDILFAPLVVPTCNTKNGLKCSSDFLTDIRSVSAYEGQYIFSIYGPSDDKVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEFPDRHPVVLVHGIYDTRAKFATMVDFLTKGGWS---VHCLDLVPNDGS--TSLALLAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-286 <WIL>
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                           13.7%;
26.1%;
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                                                                                                                                                                                                                                                                                                                Score 149; Ub .,
Pred. No. 5.7e-05;
                                                                                                                                                                                                                                                                                                                      30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 153.5; DB 2;
Pred. No. 1.5e-05;
7; Mismatches 45;
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                                                                                                                    -TDPNQKILYT----
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                                                                                                                    -SIYSSAD----
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1996
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hypothetical protein ZK617.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #tcC;Accession: T27932
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T27932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AE1975
 В
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A; Introns: 62/2
                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-344 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                             R;White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:BA000019; PIDN:BAB73309.1; PID:g17130699; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-211 <KUR>
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AE1975
                                                                                                                                                                                                                                              A; Gene: CESP: ZK617.2
                                                                                                                                                                                                                                                                                  A; Experimental source:
                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated
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                                                                                                                                          Matches
                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                   Genetics
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Best Local :
   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 LHSWMLKDFRSIEAVAAALAEPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 GHIGLIMN----SQVNSLIKEGLN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 QHPGCVQMRPNSLFLQDLNRDVQMLEQLNFTSIWTPYDLMIIPTHSSKMPVGKELTIPVA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 ALPG---TDPN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                   88 RFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIEN
                                                                                                     36 PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 KVLDE-----TGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTT---SK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPV-LSRFVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 QRNPVLLVHGITDTETVFNPMAVYLRQLGWTVYTLNLVP-----NNGEAPLNVLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alr1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QVADYVCATITPEQPFDLVGFSMGGIVSRYYVQKLGGISRVQRFVTISSPHHGTVVAYAS
   RFIETVLKYTGAQKIDVIGYSMG--
                                                                    PVVFVHGLNNEAGSLWKIARDFTNANYPRQYLFATT-WGKGTEPLNLNVAMSCTHVQHVR 123
                                                                                                                                                                                                               62/2; 121/3; 288/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                         Similarity
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                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                   EMBL: Z73897; PIDN: CAA98062.1; ce: clone ZK617
                                                                                                                                                       13.1%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.3%;
                                                                                                                                         29;
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3
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Pred. No. 8.3e
33; Mismatches
                                                                                                                                       Score 142.5; DB 2;
Pred. No. 0.00025;
9; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                      from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QKILYTSIYSSAD-MIVMNYLSKLDGAKNAQIHGV 185
SPIARKAILGGKCVDNPNVALGPSLHSRVHTYIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; 1
3.3e-05;
nes 77;
                                                                                                                                                                                                                                                                                                  GSPDB:GN00022; CESP:ZK617
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                                                                                                                                                                        Length
                                                                                                                                         57;
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                                 -WT 132
                                                                                                                                     Gaps
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A; Cross-references: EMBL: X70354
                             A; Molecule type: DNA
A; Residues: 316-358 <FR2>
                                                                       A; Title: An accessory gene, A; Reference number: $36248; A; Accession: $36248
                                                                                                                                                            A;Note: sequence extracted from NCBI backbone (NCBIN:121572, R;Frenken, L.G.J.; Bos, J.W.; Visser, C.; Mueller, W.; Tomma:
                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-358 <FRE>
                                                                                                                                                                                                                                                                                                                                                                                     R; Frenken, L.G.; Egmond, M.R.; Batenburg, A.M.; Bos, J.W.; Appl. Environ. Microbiol. 58, 3787-3791, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A48952; S36248; S37291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas glumae C; Species: Pseudomonas glumae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 3
A; Introns: 13/2; 115/2; 208/3; 268/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, August 1994 A; Reference number: Z19313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision
C;Accession: T20712
                                                                                                                                                                                                             A; Experimental source: PG1
                                                                                                                                                                                                                               A;Cross-references: EMBL:X70354; NID:g49205; PIDN:CAA49812.1;
                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                       A;Reference number: A48952;
A;Accession: A48952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:F10F2.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-300 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T20712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F10F2.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z35598; PIDN:CAA84650.1; GSPDB:GN00021; CESP:F10F2.3
A;Experimental source: clone F10F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                        Frenken, L.G.J.; Bos, J.W.
bl. Microbiol. 9, 579-589,
                                                                                                                                                                                                                                                                                                                                            Title: Cloning of the Pseudomonas glumae lipase gene and Reference number: A48952; MUID:93119130; PMID:1476423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
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nes 43; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAKAAEHNPVVMVHGIGGASY-----NFAGIKSYLVSQGWSRGKLYAVDFWDKTGT- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VAGANQGSQLCALPFFDICNMKTGLMCNSKFLEDINWFKNYEGSYKAFNLASTADFVV-G 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDGNCTLGPPLGAKVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -ENVVTLG---GANRST 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGDPVEKEPVIFIHGSGDTALFTQQPLATGFSRSIQYFLEQNYTEAELYATTWGDTWGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMLDTYSTIHTCGNLIYLRRFLEAVIGYTGAKKVDIIAHSVG----WPLMRKVVKGGTLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YL-----SKLDGAKNAQIHGVGH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YMACGKKASEFTGAHEWKVEGRNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas glumae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --NYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKI- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.8%;
                                                                                                                                            1993
                                                                                              lipB, required MUID:94018652;
                                                                                                                       lipB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 139.5;
Pred. No. 0.00
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-Oct-1999 #text_change
                                                                                              for the production PMID:8412704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
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                                                                                                                                                               Tommassen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                   determination of the
                                                                                                                                                                                                                                                                                                                                                                                                            Visser,
                                                                                                                                                                                      NCBIP:121573)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300;
                                                                                                                   of active Pseudomonas
                                                                                                                                                                                                                                  PID: 949206
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                                                                                                                                                        J.; Verrips,
                                                                                                                                                                                                                                                                                                                                                                                                          C.; Verrips,
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                                                                                                                                                                                                                                                                                                                                                                   active
                                                                                                                 glum
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; K. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.I Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reduced a;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                        Qγ
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C;Superfamily: Pseudomonas triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase; extracellular
                                                                                                                                                                                                        C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                             B69470
                                                                                                                                                                                                                                                                                                                                                                   В
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A; Accession: T24853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T12A7.4 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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                                                                                                                                                                                      C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-371 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Lennard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
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                                                                                                                                                                                                                                                  lipase homolog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 NPVVMVHGIGGA-----SYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGT-----NYN 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVTVFRLRKFVEAVMDYTGAKQINIISHSMGVTLARKVILGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATKVNLIGHSQGGLTSRYVA--AVAPQLVASVTTIGTPHRGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPVIFFHGNSDAALTANNFSTGWTTTVQYFLNQGYTLGHLYGTS-WGNTNTTAAVERDHD 169
                                                                                                                                                                                                                                                                                                                                                                   LGNKVRVILGIAGAN 240
                                                                                                                                                                                                                                                                                                                                                                                                            -GNKIENVVTLGGAN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFA-----GIKSYLVSQGWSRGKLYAVD---FWDKTGTNYNNGPVLSRFVQKVLDETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KFANVVDYWYGIQSDLQSHG---AKVYVANLSGFQSDDGPN-GRGEQLLAYVKQVLAATG
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48; Conserv
                                                                                                                                                                                   в69470
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                                                                                                                                                                                                                                                  - Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:Z73911; PIDN:CAA98139.1; GSPDB:GN00022; CESP:T12A7.4
ce: clone T12A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166/2; 218/1; 261/3; 318/1; 343/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.6%; Score 137.5; DB 2; 30.4%; Pred. No. 0.00071; wismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.8%;
29.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 139.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GANTPYYIKNLDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
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                         sulfate-reducing
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                                                                                                                   McDonald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A:Introns: 80/3; 123/2; 166/1; 200/2
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Du, Z.; Graves, T.; Gibson, A.
submitted to the EME Data Library, July 1998
A;Description: The sequence of Caenorhabditis elegans
A;Reference number: Z21322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C09E8.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-474 <KLE>
A;Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T33322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: CESP: C09E8.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                               17 LSVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YDTISWALVVETDMLFSGLGSEFGLNISQIIDPETLDKILSKSRERLIDETFSRLDRVID
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SHVFSIFSTAD
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                                                            ----SIYSSAD 164
                                                                                                                     EILGAPLTELVDTFLSVAGANYGSVLCILPVPVGTCNKKNGLHCDSEFLQDINNQHRYEG
                                                                                                                                                                                                                                                                                                                                                                                   LGMDASFGGKENPTEVPQNPVIIVHGITNKASRFGGTVAYLKSKGYKNSEIYGTTWGDSG 105
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                                                                                                                                                                                                                                                    RTPVGLVDMKCNYVKQIRAMIIAVRQYTGQKVDVIGYSMG---SPLARKAILGGQCVDTR
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se: strain Bristol N2; clone C09E8
233
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24.1%;
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21.7%; Pred. No. 0.0
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                                                                                                                                                                                    GANRSTTSKALP --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 131; DB 2; Pred. No. 0.0018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 292;
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A;Title: Genome Sequence and Comparative Analysis of the A;Reference number: A96900; MUID:21359325; PMID:21359325 A;Accession: A97027
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C;Superfamily: Pseudomonas triacylglycerol lipase
C;Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas cepacia
C:Species: Pseudomonas cepacia
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-
В
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A; Residues: 1-479 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                          A; Gene:
                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001437; PIDN:AAK79004.1; PID:g15023939; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-364 < JOR>
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Matches 51
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Best Local Similarity
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                                                                                                                                                                 166 LNIAKRFIVGFVCF--IPIINIFAMLYACHTAKIEYDHDLYKVITNKERVDSHVCKTKYP
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les 51; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 VMTLATTHAAMAATAPAAGYAATRYPIILVHGLSGTD-KYAGVLEY-----WYGIQEDLQ
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LQIIKETGCEKVNIIAHSKGGLDSRYMVSKLEMGKYVASLTMMSSPHRGCKFVDIACKIP 337
                                     QKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSKALPGTDP 150
                                                                             LVLVHGVGFRDLKYINYWGRIPKELIRNG---ATIYYGNQEAW--
                                                                                                                     VVMVHGIGGAS---YNFAG-IKSYLVSQGWSRGKLY--AVDFWDKTGTNYNNGPVLSRFV
                                                                                                                                                                                                         MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA----EHN---
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Pred. No. 0.0029;
                                                                                                                                                                                                                                                                         Score 130; DB 2; Pred. No. 0.0041;
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E.V.; Smith, D.R.
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PMID:1987151
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                                                                               GTVEYNAQYMKNKI 277
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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732.748 Million cell updates/sec
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P26877 pseudomonas
P76397 pseudomonas
P75056 mycoplasma
P41832 saccharomyc
P08658 pseudomonas
P77044 escherichia
P10335 staphylococ
Q45752 bacillus th
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   SPECIES=P.glumae;
MEDLINE=93119130;
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Burkholderia.
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Verrips C.T.;
"Cloning of the Pseudomonas
the active site residues.";
                                                                                                             DISULFID
                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                         Hydrolase;
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RESULT 3
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RC STRAI
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RT Clonn
RT Cepac
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RA FILL
RA J. Ba
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RA SCHIC
RI STUG
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01-FEB-1996
15-JUN-2002
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MUTAGEN
CONFLICT
SEQUENCE
                                                                                                                                                                                    Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T Schmid R., Schomburg D., Rydel T.J., Oliver J.D., Dunaway C.M., Larson S.B., Day J., McPherson A.; "The open conformation of a Pseudomonas lipase.", Structure 5:187-202(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, sequence, and exp
cepacia: lipase production
                                                         This SWISS-PROT entry is copyright. between the Swiss Institute of Biol
                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY.
MEDLINE=97184685; PubMed=9032074;
                                                                                                                                                                                                                                                                                                                             cepacia reveals a highly open conformation
                                                                                                                                                                                                                                                                                                                                           "The crystal structure of a triacylglycerol
                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE-97184684; PubMed-9032073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91100343; PubMed=1987151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DSM 3959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND
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              modified
                                                                                                                                                                                                                                                                                                    Structure 5:173-185(1997).
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                            European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                             CATALYTIC ACTIVITY: Triacyl fatty acid anion.
COFACTOR: REQUIRES CALCIUM.
SIMILARITY: BELONGS TO THE
                                                                                                   SIMILARITY:
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                                                                                                                 LIPASE FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                           n S., Skov K.W., Diderichsen B.;
sequence, and expression of a lipase gene from Pseudomonas
lipase production in heterologous hosts requires two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteobacteria;
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H->A:
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                                                        Bioinformatics
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1 lipase from Pseudomonas
in the absence of a bound
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                                                                                                                                                                                                                               T., Hecht H.-J.,
Strickland L.C.
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              and
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RESULT 4
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AC P1549
DT 01-AP
DT 15-JU
DT 15-JU
DT Lacto
GN LIPA
OS WIDTL
OS WIDTL
RN [1]
RP SEQUE
RC STRAI
RA Alm LA
RT Che E
RI He E
RI [2]
RP SEQUE
RC STRAI
RA MADDI
RA SELIN
RA BLILI
RA GILI
RA GILI
RA HODOI
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01-APR-1990 (Rel. 14, Created)
15-JUL-1998 (Rel. 36, Last sequence updi
15-JUN-2002 (Rel. 41, Last annotation u
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SEQUENCE
SEQUENCE FROM N.A.

STRAIN-EI TOR N19561 / Serotype 01;

MEDLINB-20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                  Alm R.A., Manning P.A.; "Characterization of the hlyB gene and its it the El Tor haemolysin of Vibrio cholerae Ol Mol. Microbiol. 4:413-425(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=El Tor O17 / Serotype O1;
MEDLINE=90286918; PubMed=2162464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae.
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                                                                                                                                                                                                                                                                        Manning P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lactonizing lipase precursor (EC LIPA OR HLYC OR VCA0221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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Pred. No. 0.0024;
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PIR; S08007; PIR; S15911;
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P25275;
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01-MAY-1992
15-JUN-2002
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InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_si
Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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Nature 406:477-483(2000)
                                 SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=92118328; PubMed=1368739;
                                                                   Pseudomonas sp. (strain F
Bacteria; Proteobacteria.
                  Fukase
                                                           NCBI_TaxID=311;
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        "Cloning, nucleotide
                         Iizumi
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SIMILARITY: STRONG, TO
SIMILARITY: BELONGS TO
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CATALYTIC ACTIVITY: Triacylglycerol +
lipase
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VCA0221; -
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THE ABHYDROLASE
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Pred. No. 0.
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Matches 42
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ACT_SITE
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                                                                                                                                    Mycoplasma pneumoniae
Bacteria; Firmicutes;
NCBI_TaxID=2104;
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01-NOV-1997 (Rel. 35, Last
16-OCT-2001 (Rel. 40, Last
Putative esterase/lipase 2
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SIGNAL
"Complete sequence analysis of the genome of the bapneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-i- SIMILARITY: BELONGS TO THE LIP3/BCHO FAMILY OF
                                                                  SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE=97105885; PubMed=89,
Himmelreich R., Hilbert H.,
                                                                                                                                                                                MPN473 OR MP368.
                                                                                                                                                                                                                                                  ESL2_MYCPN P75311;
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PIR; JQ1227; JQ1227.
HSSP; P22088; 3LIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00561; abhydrolase;
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InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPASE FAMILY. SIMILARITY: BELONGS TO THE ABHYDROLASE
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SIMILARITY: BELONGS
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PubMed=8948633;
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Pred. No. 0.0043;
B; Mismatches 5
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Signal.
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(BY SIMILARITY).
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Q02510;
Q1-JUN-1994
                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Glycerol ester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a licence accordance.
                         PIR; A47705; A47705.
InterPro; IPR000734; Lipase.
InterPro; IPR000379; Ser_estrs_site.
TIGREAMS; TIGR01168; YSIRK_signal; 1.
                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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              TIGRFAMS; TIGR011 PROSITE; PS00120;
                                                                                                                                                                                                                                                                                                                                                                                          Farrell A.M., Foster T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Serine esterase; ACT_SITE 28 POTENTIAL.
ACT_SITE 96 96 CHARGE RELAY SYSTEM (
                                                                                    EMBL; M95577; AAA19729.1; -.
                                                                                                                                                                                                                                                                                                                                                           epidermidis."
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93171870; PubMed=8436947;
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                                                                                                                                                                                                                                                                                                                                                                         "Molecular analysis and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.,
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                                                                                                                                                                                                                                                                                                                                              Gen. Microbiol. 139:267-277(1993).
                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = diacylglycerol
                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
                                                                                                                                                                                                                                                                     MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPA: NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Secreted.
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PF00561; abhydrolase; 1.
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degradation;
               LIPASE_SER;
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32.7%;
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CHARGE RELAY SYSTEM (BY SIMILARITY)
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Pred. No. 0.
Zymogen;
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Signal
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                                        EMBL; M66060; AAA21950.
PIR; D42462; D42462.
                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                               acetyldihydrolipoamide.
-!- COFACTOR: THE E2 COMPONENT CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Priefert H., Hein S., Krueger N., Zeh K., Schmidt "Identification and molecular characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OSTRAIN-H16 / DSM 428 / ATCC 17699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alcaligenes eutrophus (Ralstonia eutropha).
Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACOC_ALCEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91286190; PubMed=2061286;
                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=510;
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INDUCTION: BY GROWTH ON ACETOIN.
SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
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                 P20708;
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CHARGE RELAY SYSTEM (BY SIMILARITY).
; 70A92F25834B9E31 CRC64;
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IPR003089;

AB_hydrolase

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIP_PSEAE
P26876;
01-AUG-1992
01-APR-1993
15-JUN-2002
protein.
Biochim.
[4]
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InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92381478; PubMed-1512563; Wohlfarth S., Hoesche C., Strunk ( "Molecular genetics of the extrace aeruginosa PAOI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00364; biotin_lipoy1; Ffam; PF00561; abhydrolase; 1. PRINTS; PR00311; ABHYDROLASE. PROSITE; PS00189; LIPOYL; 1.
                                                                              Jaeger K.-E., Adrian F.-J.,
                                                                                                                                         SEQUENCE FROM N.A., AND
                                                                                                                                                                                                     Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                  MEDLINE=92337414;
Chihara-Siomi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                   MEDLINE=92247813;
                                                                                                                          STRAIN-PAC1R
                                                                                                                                                                                                                        "Purification, molecular cloning,
                                                                                                                                                                                                                                               Chihara-Siomi M., Yoshikawa K., (
Sogabe Y., Nakatani T., Nishioka
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas
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                                                           "Extracellular lipase from
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40; Conser
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                   Biophys.
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IPR000089; Biotin_lipoyl.
IPR003016; Lipoyl.
IPR000379; Ser_estrs_site.
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                                                                                                                                                                                  Biophys.
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41,
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                                                                                                   PubMed=1576157;
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                                                                                                                                                                                                                                                                                     PubMed=1632642;
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Last annotation update)
ecursor (EC 3.1.1.3) (Tr
                   1120:315-321(1992)
                                                                                                                                           SEQUENCE
                                                                                                                                                                                  296:505-513(1992).
                                                                                                                                                                                                                                                                                                                                PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                               Strunk C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision;
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                                                       , Meyer H.E., Hancock R.E.W., Pseudomonas aeruginosa is an
                                                                                                                                                                                                                                                                                                                                                                                                              extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
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; 9D5CE1F83E94892F CRC64;
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5; Mismatches
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Pred. No. 2.
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                                                                                                                                                                                                                                                 Oshima-Hirayama
a T., Oda J.;
                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                         Winkler U.K.; amphiphilic
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LVLSVTSLFA---

LAIGLASLAASPLIQASTYTQTKYPIVLAHGMLGFDNILGVDYWF-GIPSALRRDG---A

MQPSAKAAEHNPVVMVHG-----IGGASYNFAGIKSYLVSQGWSRG

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Query Match
Best Local 9
  Matches
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EMBL; AB008452; BAA73128.1; --
EMBL; AX000441; CAB77076.1; --
EMBL; AE004712; AAG06250.1; --
PIR; S25768; S25768
PIR; S24160; S24160
HSSP; P22088; 3LIP
                                                                                                    CHAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., La Garber R.L., Goltry L., Tolentino E., Westbrock Waddman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";
                                                       VARIANT
VARIANT
                                                                             VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aeruginosa EF2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gilbert E.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92085040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=ATCC 15692 / MEDLINE=20437337; Pr
                                             SEQUENCE
                                                                                                                                                                        PROSITE;
                                                                                                                                                                                Pfam; PF00561;
                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Gen. Microbiol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
                                                                                                                                                 Hydrolase;
SIGNAL
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                                                                                                                                                                                                      InterPro; IPR000073; Abhydrolase.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                              nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                   FATTY AND SHOWS A MARKED SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                            LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE AB HYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                 OF TRIOLEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANHYDROUS
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  l Similarity
32; Conser
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                                                                                                                                                                        PS00120;
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                                                                                                                                                                                            IPR000379; Ser_estrs_site
                                                                                                                                                           Lipid
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  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVITY: Triacylglycerol + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYZES THE SYLORGANIC SOLVENTS
                                             AA;
                                                                                                                                                                                 abhydrolase;
                                      108
235
277
33
156
202
204
32723
                                                                                                                                                           ; LIPASE_SER;
degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=1748875;
Jones C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10984043;
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LYZES THE SYNTHESIS OF MACROCYCLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA01;
          8.1%;
                                               MW.
                                                    LACTONIZING LIPASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
K -> Q (IN STRAIN EF2).
V -> I (IN STRAIN TE3285).
Q -> H (IN STRAIN TE3285).
I -> V (IN STRAIN TE3285).
  19;
          Score 88;
Pred. No.
                                                                                                                                                           1. Signal;
                                             7DB14DF27BDE5619
ed. No. 2.6;
Mismatches
                                                                                                                                                           Complete proteome
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CELL-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXHIBITS
                      1:
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  46;
                                                                                                                                                                                                                                                                                                                                           Usage
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R
                      Length
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                                             CRC64
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WHILE ABOUT 9
  Indels
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                       311;
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Yuan Y.,
Lim R.M.,
  14;
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MBL outstation -
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RESULT 11
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01-AUG-1992
01-AUG-1992
15-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00561; abhydrolase; 1
PROSITE; PS00120; LIPASE_SER;
Hydrolase; Lipid degradation;
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A40943; A40943.
HSSP; P22088; 3LIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 27-45 MEDLINE-92011544; PubMed-1917947;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO LIPASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                             LVLSVTSLFA---MQPSAKAAEHNPVVMVHG-----IGGASYNFAGIKSYLVSQGWSRG
                                                                                                               QVYVTEV-SQLDTSEVRGEQLLQQVEEIVALSGQPKVNLIGHSHGGPTIRY
                                                                                                                                                     KLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPY
                                                                                                                                                                                                   LAIGLASLAASPLIQASTYTQTKYPIVLAHGMLGFDNILGVDYWF-GIPSALRRDG--
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                                                                                                                                                                                                                                                                                                                   Similarity
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IPR000379; Ser_estrs_site
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
                                                                                                                                                                                                                                                                                              Conservative
    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                  LACTONIZING LIPASE.
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                 Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal
  PRT;
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  415
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TEM (BY SIMILARITY).
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RESULT 12 Y045_MYCPN ID Y045_MYCPN

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15-JUL-1998
15-JUL-1998
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., RR
Riley M., Davis N.W., Kirkpatrick H.A., Goo
                                                                                                                                                                                                                                                                                 Pfam; PF00529; HlyD; 1. Complete proteome Hypothetical protein; Signal; Complete proteome
                                                                                                                                                                                                                                                                                                                  EMBL; D90845; BAA15928.1;
EccoGene; EG14056; yegM.
InterPro; IPR002215; HlyD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map."; DNA Res. 3:379-392(1996).
-I- SIMILARITY: BELONGS TO THE ACRA/ACRE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97251358; PubMed=9097040;
Itoh T., Aiba H., Baba T., Fujita
                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                        SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Science 277:1453-1474(1997)...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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366
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                                                                                                                                               58 VSQGWSRGKLYAVDFWDKTGT-NYNNGPVLSRFVQKVLD-ETGAKKVDIVAHSMGGANTP 115
                                                                                       YYIKN-----
                          SIYSSADMIVMNYLSKL-DGAK 178
                                                        NQFVNARMLVDTEQNAVVIPTAALQMGNEGHFVWVLNSENKVSKHLVTPGIQDSQKVVIR
                                                                                                                     VVQAQKAGKPLVVEAWDRTNSKKLSEGTLLS--LDNQIDATTGTIKVKARFNNQDDALFP
AGISAGDRVVTDGIDRLTEGAK
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415 }
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                Conservative
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                                                                                    -LDGGNKIENVVTLGGANRSTTSKALPGTDPNQKILYT
387
                                                                                                                                                                                                                                       HYPOTHETICAL PROTEIN YEGM; 26240DBBE0DE1A5F CRC64;
                                                                                                                                                                                             Score 87.5;
Pred. No. 4;
                                                                                                                                                                                                                                                                        POTENTIAL.
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                                                                                                                                                                                61;
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RESULT 13
BNI1_YEAST
ID BNI1_Y
AC P41832
DT 01-NOV
DT 01-OCT
DT 16-OCT
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BNI1_YEAST
P41832;
01-NOV-1995
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Bacteria; Firmicutes;
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Pfam; PF02030; Lipoprotein_8; 1.
PRINTS; PR09095; MYCMG045.
PROSITE; PS00013; PROKAR_LIPOPROTEIN;
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between the Swiss Institute of Bioinformatics and the EMBL
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STRAIN-AFCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Pred. No. 4
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  EMBL; L31766; AAA34455.1; EMBL; Z71546; CAA96179.1; EMBL; Z71547; CAA96179.1; EMBL; X92494; CAA63225.1; SGD; S0005215; BNII. InterPro; IPR003104; FH2. Pfam; PF02181; FH2; 1. SMART; SM00498; FH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or.send an email to license@isb-sib.ch).
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Lee L. Klee S.K., Evangelista M., Bound of mitotic spindle position formin Bnilp.";
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MEDLINE=96310631; PubMed=8740425;
Men-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Ferion Seconds M., Lyck R., Fleig U., Niedenthal R.K., Fighe sequence of a 24,152 bp segment from the left XIV from Saccharomyces cerevisiae between the BNI1
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SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN.
SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 3 (FH3) DOMAIN.
SIMILARITY: CONTAINS 1 DRF AUTOREGULATORY DOMAIN (DAD)
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CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and nucleotide sequence of the Pseudomonas fragi.";
Biochem. Biophys. Res. Commun. 141:185-190(1986).
-i- CATALYTIC ACTIVITY: Triacylglycerol + H(2)0 = offatty acid anion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-IFO 3458;
STRAIN-IFO 3458;
MEDLINE-87100109; PubMed=3800995;
MEDLINE-87100109; PubMed=3800995;
MEDLINE-87100109; PubMed=3800995;
MEDLINE-87100109; PubMed=3800995;
MEDLINE-97100109; PubMed=3800995;
MEDLINE-971000009; PubMed=3800995; PubMed=3800995; PubMed=3800995; PubMed=3800995; PubMed=3800995; PubMed=3800995; PubMed=3800995; PubMed=3800
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STRAIN-IFO 12049;
MEDLINE-89078617; PubMed-3060375;
Aoyama S., Yoshida N., Inouye S.;
"Cloning, sequencing and expression of pseudomonas fragi IFO-12049 in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIP_PSEFR P08658;
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DOMAIN
EMBL; M14604; AAA25879.1; EMBL; X14033; CAA32193.1; PIR; A26383; A26383.
                                                                                                                   the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AN-1988 (Rel. 06, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lipase precursor (EC 3.1.1.3) (Triacylglycerol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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POLY-GLU.
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STRAIN-K12 / MG1655;

Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., D

Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew

Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-!- PATHWAY: 3-hydroxyphenylpropionate degradation.

-!- SIMILARITY: STRONG, TO B.CEPACIA AND PSEUDOMONAS BPHD.
                                                                                                                                                                                                                                                                                                                                                                                                MHPC_ECOLI STANDARD; PRT; 293 AA. P77044; P71204; P77205; 01-NOV-1997 (Rel. 35, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 2-hydroxy_6-ketonona-2,4-dienedioic acid hydrolase
       This
                                                                                                                                                Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., R Gregor J., Davis N.W., Kirkpatrick H.A., Go Mau B., Shao Y.;
                                                                                                                                                                                          STRAIN=K12 / MG1655; MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=K12 / CS520
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                SEQUENCE FROM N.A
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       SWISS-PROT entry
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IPR000734; Lipase.
IPR000379; Ser_estrs_site
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A., Garcia
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       is copyright.
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Search completed: May 9, 2003, 16:21:19 Job time: 15 secs
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ACT_STE 90 90 BY SIMILARITY:
CONFLICT 158 158 E -> G (IN REF. 1 AND 2).

SEQUENCE 293 AA; 32585 MW; 4407DF7B90EAOE80 CRC64;
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Pfam; PF00561; abhydrolase; 1.
PR.NTS; PR00111; ABHYDROLASE.
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InterPro; IPR000073; Abhydrolase.
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Q9rsp6 deinococcus
Q9ky65 streptomyce
Q9s295 streptomyce
Q8tc83 thermoanaer
Q59644 propionibac
P73372 synechocyst
Q33969 streptomyce
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ITALV	.larity Conserva	FROM N.A. 26; , Kim H.K., C and sequenci d (FEB-2000) 232707; AAL36; IPR002918; IPR00379; IPR00379; 1PR00379; 10674; Lipase	B26. rmicutes Bacillu 17494;	(Tremblr) (Tremblr)	PRELIMINA	•	112.68 111.99 111.58 111.58 111.59 11
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OP-SAKAAEHNPVVMVHGIG	Score 771.5; DB 2; Len Pred. No. 4.6e-53; f; Mismatches 34; Ind	Lee J.K.; lipase gene from Bacillu RMBL/GenBank/DDBJ databas	.lus/Clostridium group; Bac	Created) Last sequence update) Last annotation update)	PRT; 215 AA.	ALIGNMENTS	019310 022420 022420 028511 076556 097K91 0982D71 056594 08XXN1 026594 020437 020437 020437 020437 02437 02437 02437 02437 02437 02437 02437 02437 02437 02437 0247 0247 0247 0247 0247 0247 0247 024
31GGASYNFAGIKSYL 57 1:	gth 215; els 3; Gaps 2;	s sp. B26."; es.	Bacillales;			ent.	019310 caenorhabdi 022420 caenorhabdi 028511 archaeoglob 076556 caenorhabdi 0297k91 clostridium 092471 listeria in 068551 pseudomonas 056594 vibrio chol 08xxn1 ralstonia s 022660 caenorhabdi 043962 acinetobact 020437 caenorhabdi 052614 proteus vul 016380 caenorhabdi 072172 pseudomonas 099457 oryza sativ 091762 caenorhabdi 09huz7 pseudomonas 09av57 oryza sativ 092xy5 rhizobium m 019462 caenorhabdi 09huz7 pseudomonas 09av57 oryza sativ 092xy5 rhizobium m 019463 caenorhabdi 09huz7 pseudomonas 09av57 oryza sativ 092xy5 rhizobium m 019462 caenorhabdi 09huz7 pseudomonas 09av57 caenorhabdi 09sbr0 bacillus ha 08y8f4 listeria mo 08xr3c thermoanaer 09nak1 caenorhabdi 09evc9 chloroflexu

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Bacillus licheniformis.
Bacteria; Firmicutes; Bacillus/Cl
                                                                                                    Bacillus sp. BP-6, and
Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillaceae; Bacillus.
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01-MAY-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Enzyme Microb. Technol. 28:
EMBL; AJ297356; CAB95850.1;
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                  SPECIES-Bacillus sp.
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InterPro; IPR000379; Ser_estrs_site.
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Pastor J.,
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Last
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ursor (EC 3.1.1.1) (YFIP)
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annotation update)
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                                                                                                                           group; Bacillales;
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WSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNL 12

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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Joris B., Karamata D., Kasahara Y., Klaeir Blanchard M., Klein C.,
RA Joris B., Karamata D., Kasahara Y., Klaeir Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Punnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rager M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schleich S., Schroeter R., Soffone F.,
Schin B.S., Soldo B.,
RA Sato T., Taconi E., Takagi T., Takahashi H., Takemaru K.,
Tosato V., Uchiyana S., Vandenbol H., Vannier F., Vassarotti A.,
RA Tosato V., Uchiyana S., Vandenbol M., Vannier F., Vassarotti A.,
RA Varia A., Wambler R., Wedler H., Wassarotti A.,
RA Varia A., Wambler R., Wedler H., Wassarotti A.,
                                                                      Matches
                                                                                                      Query Match
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"The Bacillus subtilis chromosome region near 78
genes enceding a new two-component system, three
                                                                                                                                           SEQUENCE
                                                                                                                                                                               Hydrolase; Signal; SIGNAL 1
                                                                                                                                                                                                               InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
                                                                                                                                                                                                                                                                         EMBL; D78508; BAA11406.1; -. . EMBL; Z99108; CAB12664.1; -.
                                                                                                                                                                                                                                                                                                         SPECIES=B.subtilis; STRAIN-168;
Kunst F., Ogasawara N., Yoshikawa H., Danchin
Submitted (NOY-1997) to the EMBL/GenBank/DDBJ
EMBL; AJ430985; CAD24006.1; *.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viari A., Wambutt R.,
Winters P., Wipat A.,
Yoshida K., Yoshikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
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MEDLINE=98044033; Pu
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                 VKRRIIALVTILVLSVTSLFAMOPSAKAAE--HNPVVMVHGIGGASYNFAGIKSYLVSQG
181:147-151(1996).
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                                                                                     Similarity
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Bertero M.G., Bessiere
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                                                                                                                                             210
                                                                      Conservative
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                                                                                                                                             AA;
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PubMed=8973323;
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PubMed=9384377;
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28
210
                                                                                                                                             22363 MW;
                                                                                     67.2%;
68.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wedler E., Wedler H., Weitzenegger Yamamoto H., Yamane K., Yasumoto K.
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                                                                    23;
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ce of the gram-positive bacterium
                                                                                                                                                                                                proteome
                                                                                     Score 731.5;
Pred. No. 6.
                                                                                                                                                                EXTRACELLULAR ESTERASE
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                                                                      .2e-50;
es 41;
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databases
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Best Local S
Matches 142
                                                                                        O9RSP6
O9RSP6;
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
Deinococcus radiodurans.
Bacterla; Thermus/Deinococcus
Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
                                                            Lipase, putative DR2078.
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"Identification and cloning
BP-6 esterases. Comparison w
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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NCBI_TaxID=1404;
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22411 MW;
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Pred. No. 5.5
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EXTRACELLULAR ESTERASE.
94088989882C6918 CRC6
                              group;
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Query Match
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Matches 61
SEQUENCE: STRAIN-83(2);
STRAIN-83(2);
MEDLINE-97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
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01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the radioresistant bacterium radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002044; AAF11628.1; --
TIGR; DR2078; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHILE 20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Noffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                STRAIN=A3(2);
Cerdeno A.M.,
                                                                                                                                                                                                                                              Brown S.P., Harris D.;
Submitted (MAY-2000) t
                                                                                                                                                                                                                                                                  STRAIN=A3(2);
Brown S.P., H
                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                       Putative secreted lipase. SCO4799 OR SCD63A.10C.
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SEQUENCE FROM
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ismatches 93;
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        genetic
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                                                Cullum
        physical map
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Best Local
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STRAIN-83(2);
STRAIN-87000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Medanhach M., Kieser H.M., Denapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Collins M., Caronin A., Braser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Kieser T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                   SCO1735 OR SCI11.24C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                          STRAIN=A3(2);
Saunders D., Harris
Submitted (JUL-1999)
                                                                                                                                                                                                           Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, Putative secreted lipase.
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Nature 417:141-147(2002).
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InterPro; IPR000379; Ser_estts_site.
PROSITE; PS00120; LIPASE_SER; 1.
SEQUENCE 331 AA; 35137 MW; 3E0E7
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                                                  SEQUENCE FROM N.A.
                                                                             Submitted (JUL-1999)
                                                                                           James K.D.,
                                                                                                                    SEQUENCE
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Microbiol. 21:77-96(1996).
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                                                                                         Parkhill
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Pred. No. 2.1
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                                      STRAIN=MB4T / JCM11007;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992817; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Hu Z., Xuan Z., Hu
Chen Y., Xua Y., Lai X., Huang L., E
Tan H., Chen R., Wang J., Yu J., Yang H.;
Ta complete sequence of T. tengcongensis ge
Genome Res. 12:689-700(2002).
EMBL; AE013025; AMA23831.1; -.
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Nature 417:141-147(2002).
EMBL; AL096849; CABS0950:1; -.
HSSP; Q05489; 1TAH.
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted acetyltransferases and hydrolases with th
hydrolase fold.
Transferase;
SEQUENCE 4
                                                                                                                                                                                                                                                                                              Thermoanaerobacteriales; NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                 Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
SEQUENCE 290 AA; 30496 MW; D56E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                     LIPA OR TTE0555.
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1. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LATKYDEVVTPYRGQFLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGANRSTT----SKALP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYSSADMIVMNYLSK-LDG
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Hydrolase; Complete
03 AA; 45221 MW; DC
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28 6%;
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Pred. No. 3
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Matches 55
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Best Local :
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01.NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Triacylglycerol lipase precursor (EC 3.1.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miskin J.E., Farrell A.M., Cunliffe W. Tropionibacterium acnes, a resident of produces a 33 kDa extracellular lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Propionibacterineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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EMBL; X99255; CAA67627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97312013; PubMed=9168624;
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SSADMIVMNYLSK-LDGAKNAQI
                                                    AVGLDKLVDGLPEAVKDFLSTWSYDHNMEAYGQQLKGSALMQQVYRDGDTVPGIAYTVIS
                                                                                                                                                           AQALGAFVDRVRKATGSEKVDFVGHSQGGGILPNAYIKMYGGASKVDKLIGLVAANHGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAGDYN 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFTFRNPNMAWGIMTTGGFGPVPYTYMLIYGLWYNTTYHSIYTEGGAYPGQLQMLARWDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKN-----LDGGNKIENVVTLGGANRS- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVVMVHGIGGASYNFA-----
                                                                                                                                                                                                          GPVLSRFVQKVLDETGAKKVDIVAHSMGGANTP-YYIKNLDGGNKIENVVTLGGANRSTT 141
                                                                                                                                                                                                                                                               PVILIPGTGGNAFATWSFYG--PHLAHEGYC---VYTFTTNVPVGILDEGWGFTGDVRAS
                                                                                                                                                                                                                                                                                                                    PVVMVHGIGG---ASYNFAGIKSYLVSQGWSRGKLYAV-----DFWDKTGTNYNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01674; Lipase_2; 1.
PE; PS00120; LIPASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
                                                                                                                                                                                                                                                                                                                                                                      Similarity 27.155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002918; Lipase_2.
IPR000379; Ser_estrs_site
1674; Lipase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
35995 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 14.8%;
27.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%;
                                                                                                         -GTDPNQK---
                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cunliffe W.J., Holland K.T.; a resident of lipid-rich human skin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                      Score 160.5; DB 2;
Pred. No. 9.6e-05;
4; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60F63DF5B5DFDBD9 CRC64;
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                      lipase
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01-FEB-1997
01-MAR-2002
                          SEQUENCE FROM N.A.
MEDLINE=97438518; PubMed=9293006;
Sommer P., Bormann C., Goetz F.;
"Genetic and biochemical characterization of a
                                                                                                                                          Streptomyces cinnamoneus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01674; Lipase_2; 1.
Hypothetical protein; Complete
SEQUENCE 202 AA; 22429 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hihara Y., Ikeuchi M.;
Submitted (JUN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K. Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechocystis sp. (strain PCC 6803). Bacteria; Cyanobacteria; Chroococcal
                                                                                                                                                                           Lipase LipA precursor.
                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D90905; BAA17403.1;
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                                                                                                             NCBI_TaxID=53446;
                                                                                                                              Actinomycetales;
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             from Streptomyces
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                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                              Streptomycineae;
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                cinnamomeus
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63:3553-3560(1997).
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                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
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Pred. No. 0.00
27; Mismatches
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Last annotation update)
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8758C3119B7352EF CRC64;
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                                                                                                                              Streptomycetaceae;
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                                                                                                                              Streptomyces
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Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
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InterPro; IPR000734; Lipase_2.
InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
                                                                                                                                                                          InterPro; IPR000734; Lipase.
InterPro; IPR002918; Lipase_2.
InterPro; IPR00379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
PROSITE; PS00120; LIPASE_SER; UNKNOW
                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; AL110484; CAB54398.1;
                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                   Wallis J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                            'Genome sequence of the nematode
                                                                                                                                                                                                                                                                                                             none;
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l-OCT-2000 (TremBLrel.
L-MAR-2002 (TremBLrel.
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                                            PVILVHGTTNSAGTFAPQAAYFRANGWSEETVYATTYGDAGVTTATNVKMLCEYVQQIRN 125
                                                                       PVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKTGTNYNNGPVLSRFVQKV-- 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CPSCVDQQAGSELLQKLNAGDETPAGPDYTVITTRYDEVVIPYASAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRGATGAAKVDIVGHSQGGMLPRYYVKFLGGADKVDDLVGIVPSNHGTKNPLAIPAGWTF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLGGANRSTTSK-ALP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRITALVTILVLSVTSLFAMQPSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YNFAGIKSYLVSQGWSRGK------LYAVDFWDKTGTNYNNGPV-----LSRFVQK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFLIAAAATAALGLTGLSA--PAAASVLDVPPGGANDWSCKPDSAHPQPVVLVNG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
58; Conser
                                                                                                     Similarity
55; Conser
 -LDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVTLG-
                                                                                                                                                                                                                                                                                                                                                                  (MAY-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 AA;
                                                                                                                                                              286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTDPNQKIL-----YTSIYSSADMIVMNYLSKL
                                                                                                                                                              AA;
                                                                                                                                                              LIPASE_SER; UNKNOWN_1.
; 29876 MW; 0117E6F4E3D73094 CRC64;
                                                                                                                                                                                                                                                                                                                         PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 F
29213 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                  13.7%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%;
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15,
20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                  Score 149; DB 5;
Pred. No. 0.00061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 152; DB 2
Pred. No. 0.0003
4; Mismatches <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A05AB4A0C984394C CRC64;
                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286
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es < 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                               Length 286;
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                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                             for
                                                                                                    55;
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               င်
                                                                                                  Gaps
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                135
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RESULT 13
Q91UYO
ID Q91UY
AC Q91UY
DT 01-DE
DT 01-TU
DE Alkal
OS uncul
OS uncul
OS UNCUL
RA BEIT
RN [1]
RA BEIT
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Prospecting for novel lipases using PC Submitted (SEP-2001) to the EMBL/GenBan EMBL, AR421494; AAL17608.1; -
InterPro; IPR000561; EGF-like.
InterPro; IPR000734; Lipase.
InterPro; IPR000734; Lipase.
InterPro; IPR000739; Ser_estrs_site.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01120; LIPASE_SER; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91UY0;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Alkaline lipase (EC 3.1.1.3).
uncultured organism.
unclassified; environmental samples.
uCBI_TaxID=155900;
                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                   Streptomyces coelicolor
                                                                                           Putative lipase.
SCO1265 OR 2SCG18.12C
                                                                                                                                          01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                      Q9K3H5;
                                                                                                                                                                                                                                                  Q9K3H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04nt6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bell P.J
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                                                                                                                                                                                                                                                                                                                                                                             238
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                                                                                                                                                                                                                                                                                                                                                                             CGAGYNVACCYVYGVHSSKPQILDGETSYSTVPYGHFGVL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PACNDHYGSELDTVKQALQQALSKSRTGMIDVMGHSMGATLAAKAILDLGIANKVRTFVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTVCGRVSRIDGATAEKDNVPGNHDAIIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTSLFAMQPSAKAAEHNPVVMVHGIGGASYNFAGIKSYLVSQGWSRGKLYAVDFWDKT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt ANRGTSLCDILFAPLYVPTCNTKNGLKCSSDFLTDIRSVSAYEGQYIFSIYGPSDDKVGF}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAGAFRGLNSCGVYPYNVPTTTCGRYGLSINSPLVNSLANKRFGKYQYAIYSWVDEIVCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAADLIIAESRLTGSQGEPVVMVHGNAGYPSNWDNTVNYFLQNGWTSDMIIRPNWGSKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GTNYNNGPVL---SRFVQKVLDETGAKKVDIVAHSMGGANTPYYIKNLDGGNKIENVVT 132
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                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31886 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          YLSK----LDGAKNAQIHGVGHIGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NRSTTSKALPGTDPNQKILYT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.6%; Score 148; DB 14; 24.5%; Pred. No. 0.00075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gibbs M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSKALPG-----
                                                                                                                                               15,
15,
21,
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                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4C6BD89AA69DD6EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR."
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                       Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SIYSSADMIVMN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
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RESULT
Q8YX63
ID Q8YX63
AC Q8
AC Q8
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DT 01
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GN ALL
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Best Local S
Matches 55
                                              QBYX63;

Q1-MAR-2002 (TrEMBLrel. 20, C)

Q1-MAR-2002 (TrEMBLrel. 21, L)

Q1-JUN-2002 (TrEMBLrel. 21, L)

Q1-JUN-2002 (TrEMBLrel. 21, L)
                                          Hypothetical ALR1352.
                                                                                                                           Q8YX63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:41-147(2002).
EMBL; AL390188; CAB99145.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherfod K., Rutter S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; nol. microbiol. 21:77-96(1996).
               Bacteria;
                           Anabaena sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002918; Lipase_2.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF01674; Lipase_2; 1.
SEQUENCE 289 AA; 31466 MW; 03D90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seeger K., Saunders D., Sharp S., Squares R., Squares S.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brown S.P., Harris D.;
Submitted (JUL-2000) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
Brown S.P., H
 NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=A3(2) / M145;
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Kinashi H., Hopwood D.A.;
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Hypothetical protein; Complete proteome.
SEQUENCE 211 AA; 23718 MW; 08A8720935DA8F75 CRC64;
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EMBL, AP003585; BAB73309.1; -.
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SUMMARIES

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                                                                                                 Bacillus
Bacillus
                                                                                                                                         Sequence
Ax418878
                                               Giver,L.J., Minshull,J.
Novel lipase genes
Patent: WO 0206457-A 8
                                       Maxygen,
                                                                                          Bacteria;
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                    Location/Qualifiers
1. 639
/organism="Bacillus k
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                                        Inc. (US)
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123 c 157 g
                                                                                        Firmicutes; Bacillales;
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86
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Patent WO0206457.
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Pred. No. 1.26
0; Mismatches
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                                                                    and Vogel, K.
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Bacillaceae;

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linear

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18-JUN-2002

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REFERENCE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wordman, S., Lathrop, S.J., Longchamp, P.F. and Whalen, R. Methods and compositions for developing spore display medicanal-apd-industrial-applications patent: wo 0200232-A 2 03-JAN-2002;

Maxygen, Inc. (US)
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                                                                                                                               Bacillus circulans
Bacillus circulans
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AX365571
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                                                                                                                       Bacteria; Firmicutes;
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  /organism="Bacillus circulans"
/db_xref="taxon:1397"
1.639
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                                            Location/Qualifiers
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Sequence 4
AX418874
                    Bacillus l
Bacillus l
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SSADMIYMNYLSKLGAKANVQLHGVGHIGLLMNSQVNSLIKEGLNGGGLNTN"
a 122 c 157 g 159 t
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Minshull,J.
                                                                GI:21523729
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98.7%;
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Pred. No. 1.2e
0; Mismatches
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                     Bacillales;
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W00206457
and Vogel, K.
                     Bacillaceae;
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PAT

18-JUN-2002

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BASE COUNT
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Sequence
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Patent: WO 0206457-A 4 24-JAN-2002;
Maxygen, Inc. (US)
 Patent:
           Novel
                    Giver, L.J., Minshull, J. and Vogel, K.
                                        Bacteria;
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Pred. No. 1.2e-180;
0; Mismatches 8;
                                        Bacillales; Bacillaceae;
 24-JAN-2002;
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                                                                                                                    Sequence
AX418876
                   Giver,L.J., Minshull,J.
Novel lipase genes
Patent: WO 0206457-A 6
                                                           Bacillus azotoformans.
Bacillus azotoformans
Bacteria; Firmicutes; Bacillales;
          Maxygen,
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/db_xref="taxon:139;
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                           Novel lip
Patent: V
Maxygen,
                                    Giver, L.J., Minshull, J. and Novel lipase genes Patent: WO 0206457-A 3 24-JF
                                                                                    Bacillus megaterium. Bacillus megaterium
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Sequence 3 from Patent WO0206457
AX418873.1 GI:21523728
                                                                            Bacteria;
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/organism="Bacillus azotoformans"
/db_xref="taxon:1454"
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                            Inc. (US)
         Location/Qualifiers
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 /organism="Bacillus
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                                                              AB000617.1 GI:2415716

YCCK; NatB; YCC6; YCCK; YCC9; Y
YCCB; YCCA; YCdI; YCdI; YCdG; Y.
NatA; YCCH; YCCG; YCCE; Y.
LmrA; YCCA; LmrB; YCbU
Bacillus subtilis
Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             632;
     Kumano,M., Tamakoshi,A. and Yamane,K.
A 32 kb nucleotide sequence from the region of the
Lincomycin-resistance gene (22-25 degree) of the Bacillus subtilis
chromosome and identification of the site of the lin-2 mutation
                                                                                                                                            cds
                                                                                                                                                     Bacillus
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Pred. No. 1.4
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22 -
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YcdF; RapJ;
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                                                        Bacillus
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Yamane, K.
Direct Submission
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GGILLSLTAKNSTPLLHISSCIPDLLKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIMVFICMMVILSSMLLLPMYLQGGLVLTÄFASGLVLLPGGILNGFMSPVTGRLFDKY
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PREFYPDGTALMNTLQQMAGALGTAVAVSIMAAGQHDYMSTVKNPADPAVIPQALTAG
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pyridoxal-phosphate-dependent aminotransferase"
                                                                                                                                                                                                                                                                                                                                                             probable repressor of lincomycin-resistance operon*
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3225.
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VQDIKAIAEISQRKGSLLFVDAYQSAGHIPIDVKEWGVDMLAAGTRKYLLGIPGVAFL
YVRKELADALKPKASAWFGRESGFDGAYAKVARREQTGTPAFISVYAAAAALSLLNHI
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'note="probable L-asparaginase
                         'gene="yccc"
                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                      'note="lmrA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="yccB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="
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precursor"
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/gene="y
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/note="homologue of sensor/response regulator protein of
Staphylococcus aureus"
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VVIVGSMRPSTAISADGPSNLYNAVKVAGAPEAKGKGTLVVLNDRIASARYVTKTNTT
                                                                                                                                                        complement(8677.
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NGAHEGMGTYIIQKLVKGAFGRLDFTYRHPIFRLEIKIPFQK"
                                                                                                                                                                                                                                                    DQYSQYDRFLKGENAYVAGVLYDFLEKARASNVSVSLHMHTPLSSLPFSPADQVSLVG
                                                                                                                                                                                                                                                                                 YIWNTKRVWKHCSSGLCAWIAVIQVMSVGVVLIGTDIMPVLCVIAIFAGCEGLRIGOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSRYKEIESTLQDEADRFAQALSS*
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PAVIDIWKTFCEKKSPVIRKPEAFAAAVEYYVNAISLNGASVSQAKLAKKYGVSASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLPPVGSLILGYPIHEAEKAEFFMQFTIFPVKRTEALISKVKKYADAAVKDGKTPEDF
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/protein_id="BAA22231.1"
/db_xref="GI:2415721"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MKKQRMLVLFTALLFVFTGCSHSPETKESPKEKAQTQKVSSASA
SEKKDLPNIRILATGGTIAGADQSKTSTTEYKAGVVGVESLIEAVPEMKDIANVSGEQ
                                                                                                                        /gene="yccH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YAEKDLLASNSLNPQKARMLLMLALTKTNDPQKIQAYFNEY"
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/protein_id="BAA22230.1"
/db_xref="GI:2415720"
                                                                                                                                                                                                                                                                                                                                          translation="MITLFQCLYLILFSFICYQGAAAFSHSTAASWLAAALGAAAAGL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                              CTGGACGGCGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACG
                                                                                                                                                                                                    AAAGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACACCTTACTACATAAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG 180
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                                                                                                                                                                                                                                                                    AACAATGGACCGGTATTATCACGATTTGTGCAAAAGGTTTTAGATGAAACGGGTGCGAAA
                                                                                                                                                                                                                                                                                           AACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAA
                                                                                                                                                                                                                                                                                                                                                        CACGGTATTGGAGGGGCATCATTCAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
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                                                                                      CTGGACGGCGGAAATAAAGTTGCAAACGTCGTGACGCTTGGCGGCGCGCAACCGTTTGACG
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/TIMLRMIASLLEPSQGVITVDGFDTVKQPAEVKQRIGVLFGGETGLYDRMTAKENLQY
FGRLYGLNRHEIKARIEDLSKRFGMRDYMNRRVGGFSKGMRQKVAIARALIHDPDIIL
FDEPTTGLDITSSNIFREFIQQLKREGKTILFSSHIMEEVQALCDSVIMIHSGEVIYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="natA"
9522. .10262
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/db_xref="G1:2415725"
/db_xref="G1:2415725"
/translation="mykyGLVDDYRVDLEKLEAIVSRMQDVEIVFSTDSAKEAYRRVK
NGDIDLLLADIEMPHMSGYELADLIKSHSLDVDVIFVTGHGGYAVHAFDLNVHDYIMK
PYYADRLAASFDRYLKKKTETSLNGRILIKQKSEMHVLQKKDIIFAERTGRSTTIVTT
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/gene="natB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MLSAILPMLILTSIVSGAMPIALDIMAGEKDRKSIEALLLTPVS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAA22237.1"
/db_xref="GI:2415727"
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/transl_table=11
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/db_xref="GI:2415726"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="homologue of ATP-binding transport protein (function unknown) of Bacillus subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="NatB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="function of NatB is not known, Integral membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="NatA"
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Pred. No. 3.8e-164;
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/organism="Bacillus subtilis" /strain="168"

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Azevedo, V. Bertero, M.G. Bessleres, P., Bolotin, A., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Brorriss, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Broursier, N.M., Chois, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Chois, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Chois, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Ehrlich, S.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, W., Fujita, W., Fujita, W., Fujita, W., Fujita, W., Galizzi, A., Galizzi, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAAACGCT
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                                                                                                                                                         Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Paster Regulation de l'Expression Genetique, 28 rue du Docteur Roux,
                                                              Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, F 68 89 48
                                                                                                                                                                                                                                                              2 (bases 1 to 221160)
Kunst, F., Ogasawara, N.,
                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                              The complete genome sequence of the gram-positive bacterium Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 221160)
Kunst, F., Ogasawara, N.
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Location/Qualifiers
1. .221160
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                                                                                                                                                                                                                                                              Yoshikawa, H. and Danchin, A.
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GLSSSQNIEFLDPESQAIDVTAKGSPTNINKLKKSDIELYVNVSDLEDGEHSVKLEVN
GPQNVTWSLGRKNAKIKLTSKKSNTSTNDNSSNTSGNQDTDKQTNDQKNNQQEDTKNT
                                                                                                                                                                                                                                                                             /translation="MDKFLNNRWAVKIIALLFALLLYVAVNSNQAPTPKKPGESFFPT
STTDEATLTDLPVKAYYDDENVVTGVPQTVNVTIKSGTSAVKARQTRNFEIYADME
HLKTGTHKVELKAKNVSDGLTISINFSVTTVTJQERTTKSFPVEVEYYNKSKMKKYS
PEQPTVSPKNVQITGSKNVINNISLHKASVNLENADETEKEAKVTVYVDKDGNALPVD
VEPSVIKITVPVTSPSKKVPFKIERTGSLPDGVSIANIESSPSEVTVYGSQDVLDSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="
1552. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="Sptrembl:Q45588"
/taanslation="MSCPEQIYQLMHMHLDGDILPKDEHYLNEHLETCEKCRKHFYEM/Translation="MSCPEQIYQLMHMHLDGDILPKDEHYLNEHLETCEKCRKHFYEM/EXSALPKEKRASVKRWFRTHFVIAAAAVFIILMGGEKSTALVRSVSHVBABAAVFIILMGGFTNKMGHLTIKGKIDGDVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MEMMIKKRIKQVKKGDQDAFADIVDIYKDKIYQLCYRMLGNVHE
AEDIAQEAFIRAYVNIDSFDINRKFSTWLYRIATNLTIDRIRKKKPDYYLDAEVAGTE
GLTMYSQIVADGVLPEDAVVSLELSNTIQQKILKLPDKYRTVIVLKYIDELSLIEIGE
                                                                                                                                                                       DKNNNDQNQDGNKDQNQDQDEDESTANSQSSSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q45589"
/translation="MAFEDIPFLQYLGNAVDILLVWYVIYKLIMVIRGTKAVQLLKGI
VVIVLVRWASQYLGLSTLQWLMDQAITWGFLAIIIIFQPELRRALEQLGRGRFFSRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="alternate gene name: ybbQ
similar to hypothetical proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNGEKYMASAGQVTGQIEEINQLFDWTWYKMKSAGKSVLDAFNPNGEE'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIFIPNTPLHDGAVIMKNNEIAAAACYLPLSESPFISKELGTRHRAAVGISEVTDSLT
IIVSEETGGVSVAKNGDLHRELTEEALKEMLEAEFKKNTRDTSSNRWYWRGRKNG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPVEEAQQKTIEAITKAINYMAKRRIGALLTIERDTGMGDYIETGIPLNAKVSSELLI
                                                       /gene="ybbT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB11969.1"
/db_xref="GI:2632461"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/protein_id="CAB11967.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="RNA polymerase ECF-type sigma factor (sigma-W)"
/protein_id="CAB11966.1"
'note="similar to phosphoglucomutase (glycolysis)"
                          function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                             'db_xref="SPTREMBL:034659"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="ybbR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:2632460"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'protein_id="CAB11968.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="ybbP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="GI:2632459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ybbM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [LNIPVGTVKTRIHRGREALRKQLRDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="SPTREMBL:Q45585"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="sigW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="unknown"
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. 2373
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.2373
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Query Match
Best Local Similarity
Matches 598; Conserv
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(7883. .8794)
/gene="alkA"
/EC_number="3.2.2.21"
                                                                                                                                                                 /translation="MTWHEYNDVIVITLPEIFDMNANLGYLTREKNECMYEIENNITT
KVIAJGEIRSLYQVSVINNKOMIVQFLNDSRFVEQMKREEIVRYKIHEWFDLDNDLTPF
YEMAKAADPLLKMPARKFYGLEVIGJEDLFEALCWGVLGQGINLAFAYSLKKQFVEAFG
DSIEWNGKKYWVFPPYERIARLTPTDLADIKMTVKKSEYIIGIARLMASGELSREKLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(7883.
/gene="alkA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIAREYLTVSRNAFFIGRGLDYFVCVEGALKLKEISYIQAEGFAGGELKHGTIALIEQ
GTPVFALATQEHVNLSIRGNVKEVAARGANTCIIŞLKGLDDADDRFVLPEVNPALAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mCGIVGYIGQLDAKEILLKGLEKLEYRGYDSAGIAVANEQGIHV
FKEKGRIADLREVVDANVEAKAGIGHTRWATHGEPSYLNAHPHQSALGRETLVHNGVI
ENYVQLKQEYLQDVELKSDTDTEVVVQVIEQFVNGGLETEEAFRKTLTLLKGSYAIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="L-glutamine-D-fructose-6-phosphate
amidotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="glmS"
5613. .7415
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THPEALSAFVKEKNADLGLAFDGDGDRLIAVDEKGNIVDGDQIMYICSKHLKSEGRLK
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IGRDTRISGHMLEGALVAGLLSIGAEVMRLGVISTPGVSYLTKAMDAEAGVMISASHN
                                                                                                               KDEILEISVPWKEWQSYATFYLWRVLY"
                                                                                                                                         KMNFKDAEKNLIKIRGIGPWTANYVLMRCLRFPTAFPIDDVGLIHSIKILRNMNRKPT
                                                                                                                                                                                                                                                                                                       /product="DNA-3-methyladenine glycosylase"
/protein_id="CAB11973.1"
/db_xref="GI:2632465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB11972.1"
/db_xref="GI:2632464"
/db_xref="SPTREMBL:034568"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="glms"
7462. .7602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSVVPLQLIAYYAALHRGCDVDKPRNLAKSVTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIAVASTKAYTÄQIAVLAVLASVAÄDKNGINIGFDLVKELGIAANAMEALCDQKDEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSKKPLFIFLSQSGETADSRAVLVQVKALGHKALTITNVPGSTLSREADYTLLLHAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSVPGDIAAAVAEADRIYIIGCGTSYHAGLVGKQYIEMWANVPVEVHVASEFSYNMPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVIKNLDGDVITRASYIAELDASDIEKGTYPHYMLKETDEQPVVMRKIIQTYQDENGK
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/db_xref="GI:2632462"
                                                                                                                                                                                                                                                                                /db_xref="SWISS-PROT:P37878"
                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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7462. .7602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB11971.1"
/db_xref="GI:2632463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="alternate gene name: gcaA, ybxD"
                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="adaptative response to DNA alkylation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="ybbU"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="glms"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="SPTREMBL:034824"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
                       89.7%;
0;
                       Score 573.4; DB 1; Pred. No. 5.3e-164;
Mismatches
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Indels
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221160; 0,

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97109

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                                               -35_signal
         -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACG
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Dartois, V., Baulard, A., Schanck, K. and Colson, C.
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92329538
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Bacillus subtilis (strain
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                                                                                             /organism="Bacillus subtilis"
/strain="W168"
/db_xref="taxon:1423"
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DIVAHSMGGANTLYXIKULDGGNVANVVTVGGANRLTTGKALPGTDPDWKILYTSIY
SSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN"
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/EC_number="3.1.1.
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Vandamme, E., Schanck-Brodrueck, K.H., Colson, C. and Hanotier, DNA segment coding for a specific lipase, vectors for the expression thereof, microorganisms transformed by these vectouse of these microorgenisms for the production of the lipase Patent: EP 0243338-A 1 28-OCT-1987;
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                                                     AAAGTGGATATTGTCGCTCGCAGCATGGGGGGGCGCGAACACACTTTACTACATAAAAAAT
                                                                  AAAGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACACCCTTACTACATAAAAAAT
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1 (bases 1 to 1831)
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GapfnfagtksypvsQGwsrdklyavdfwdktgtnynngpvlsrfvQkvldetgakkv
DivarswGGantlyyiknldggnkvanvvtlgganrlttgkalpgtdpnQkilytsiy
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/db_xref="taxon:32630"
165. .170
192. .197
203. .841
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367 c 416 g 463 t
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/protein_id="CAA00274.1"
/db_xref="GI:412318"
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/transl_table=11
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92.8%;
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Pred. No. 6.2e-162;
0; Mismatches 46;
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          CTGGACGCCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACG
                              AACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAA 300
                                                                                                                                 GGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
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artificial sequences.

1 (bases 1 to 1831)
Vandamme, E., Schanck-Brodrueck, K.H., Colson, C. and Hanotier, J.D.V.
DNA segment coding for a specific lipase, vectors for the
expression thereof, microorganisms transformed by these vectors and
use of these microorgenisms for the production of the lipase
Patent: EP 024338-A 4 28-OCT-1987;
FINA RESEARCH 5.A.
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/db_xref="taxon:32630"
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AACAATGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAA 300
                                                                                                                                                                               ACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC 480
                                                                                                         GGCTGGTCGCGGGACAAGCTGTATGCAGTTGATTTTTGGGACAAGACAGGCACAAATTAT
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                                                                      AACAATGGACCGGTATTACCACGATTTGTGCAAAAAGGTTTTAGATGAAACGGGTGCGAAA
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Bacillus
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Sequence
AX418872
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/db_xref="taxon:1423"
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Patent WO0206457
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Pred. No. 1e-161;
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     100.0
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _Geneseq_101002:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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_	Ва	ABK33857	24	544	7.	92.	ũ
illus lipa	Bac	ABK33855	24	544	7.		N
_	Ba	ABK33854	24	544	7.	94.	
8		ABK33850	24	544	7.	9	0
illus lipa		ABK33866	24	544	8	99.	9
illus lipa	Bac.	ABK33847	24	544	8		œ
_	Вас	ABK33869	24	544	8.	00.	7
_	Bac	ABK33868	24	544	8	50	6
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_	Вас	ABK33849	24	544	9.	05.	4
_	Вас	ABK33846	24	544	9.	05.	w
_	Bac	ABK33840	24	544	9.	05.	N
lus 1:	Bac	ABK33839	24	544	9	07.	Н
illus l	Bac	ABK33867	24	544	9.	08.	0
illus l	, Bac	ABK33860	24	544	9.	08.	9
illus l	Bac	ABK33832	24	639	9.	09.	8
illus 1	Bac	ABK33848	24	544	79.9	510.4	7
illus l	Bac	ABK33841	24	544	9.	10.	6
illus l	Bac	ABK33851	24	544	0	51	5
illus l	Bac	ABK33833	24	639	0.	12	4
illus 1	. Bac	ABK33834	24	639	0.	14.	w
illus l	Bac	ABK33870	24	544	0	٠	N
-	Вас	ABK33862	24	544	0	15.	1
_	Bac	ABK33852	24	544	0	15.	0
_	Bac	ABK33858	24	544	0	16.	9
llus l	Bac	ABK33863	24	544	<u>.</u>	18.	8
۳.	Bac	ABK33844	24	544	-	18.	7
illus lipa	Вас	ABK33864	24	544	۲.	21.	9
s H	. Вас	ABK33861	24	544	۲.	21.	Ç,
s L		ABK33872	24	544	۳.	23.	4
us 1:	Bac	ABK33871	24	544	<u>'</u>	23.	w
us 1:	Ва	ABK33842	24	544	1	23.	2
illus lipa	Вас	ABK33827	24	639	8	62.	_
illus lipa	Ва	338	24	639	8	64.	0

ALIGNMENTS

RESULT 1
ABK33819
ID ABK3

ABK33819 standard; DNA; 639

ВP

Bacillus lipase polynucleotide #1.

08-MAY-2002 ABK33819;

(first entry)

Giver LJ, Minshull J, 13-JUL-2000; 21-JUN-2001; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory; 13-JUL-2001; 2001WO-US22160 24-JAN-2002 WO200206457-A2 Bacillus pumilus. (MAXY-) MAXYGEN INC gastrointestinal Lipase; Bacillus; animal feed; 2000US-217954P. 2001US-300378P. Vogel K; flavour modification; fat modification;

Bacillus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase polynucleotides of the invention.
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CAAATTCATGGCGTTGGGCACATTGGTTATTGATGAACAGCCAAGTCAACAGCCTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAAGACACGAATTAT
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                                                                                                                                                                                                                                                   CTGGACGGCGGAAATAAAATTGAAAACGTCGTAACGCTTGGCGGCGCGAACCGTTCGACG
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                                                                                                                                                                            ACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTAC
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al feeds, as agents of flavour modification and
disease and coeliac disease -
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Pred. No. 4.2e-190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 81;
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21-JUN-2001;
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les 633;
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animal feeds, as agents of flavour modification and for treating
ohn's disease and coeliac disease -
CACGGTATCGGAGGAGCTTCATACAATTTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
                                                                  TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
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DB; AAU83847.
                                                     TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
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2001US-300378P
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                                                                                                                                                                Score 629.4; DB 24; Pred. No. 4.3e-187; 0; Mismatches 6;
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RESULT 3
ABK3 382/6
ID ABK3
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ID ABK3
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XX DT 08-1
DT 08-1
DT 08-2
XX Lip
KW Lip
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KW 99as
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                      Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
                                                                                                                                                                                                                                        (MAXY-) MAXYGEN INC
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning
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Local Similarity 98.9%;
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                                                                                                                   AGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGCT
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                                                    CAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATT
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Pred. No. 1.4e-186;
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21-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic
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                                                                                                                                                                   TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
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                                         GGCTGGTCACGGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
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ng; cleaning agent; Crohn's disease; cystic fibrosis;
indigestion; obesity; gastrointestinal mal-absorption;
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Pred. No. 4.3e-186;
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gastrointestinal
                            coeliac
                                                                                             Bacillus lipase polynucleotide #5.
                                                                                                                        08-MAY-2002
                                                                                                                                                   ABK33823;
               gastrointestinal
                                                                    Lipase;
                                           leather
                                                                                                                        entry)
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Bacillus circulans e; Bacillus; animal feed; flavour modification; fat modification; foodstuff; cheese; food emulsifier; leather tanning; gene; ds; er processing; cleaning agent; Crohn's disease; cystic fibrosis; ac disease; indigestion; obesity; gastrointestinal mal-absorption; ointestinal lipid related condition; antiinflammatory; respiratory;

24-JAN-2002 WO200206457-A2

13-JUL-2001; 2001WO-US22160

13-JUL-2000; 21-JUN-2001; 2000US-217954P. 2001US-300378P.

(MAXY-) MAXYGEN INC

Minshull Vogel ζ.

2002-171805/22. DB; AAU83845.

Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease for supplements r treating

Claim 81; Page 118-119; 196pp; English.

The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning. ç 10 in

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Best Local S
Matches 631
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 autoimmune
gene; ds.
                      Lipase 396;
                                             Bacillus
                                                                  16-APR-2002
                                                                                          ABA96150;
                                                                                                               ABA96150
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                                           circulans lipase
                                                                                                              standard;
          ; spore protein application; immune response; HIV; cancer; disorder; inflammatory; allergic reaction; autoantigen:
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98.7%;
                                                                 entry]
         inflammatory; allergic
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Pred. No. 4.3e-186;
                                           gene
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Best Local S
Matches 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intion for modulating immune response, of a spore and polypeptide, carbohydrate anti-pathogenic activity
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/product= "lipase
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 626.2; DB 24;
Pred. No. 4.3e-186;
Pred. No. 4.3e-186;
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e or nucleotide sequence
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RESULT 7
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The invention relates to new Bacillus lipase enzymes and the nucleic acids encoding them. The lipase polypeptides are useful as supplements in animal feeds, as agents of flavour modification and fat modification in human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, coeliac disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
                                                                                                                                                                                                           Claim 81; Page 119; 196pp; English.
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21-JUN-2001; 2001US-300378P
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animal feeds, as agents of flavour modification and
ohn's disease and coeliac disease -
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                   Bacillus megaterium
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Pred. No. 4.4e-1
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Matches 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
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21-JUN-2001; 2001US-300378P.
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                                                                                                                                                                                                                                                                               CAC-GGTATCGGAGGAGCTTCATACAATTTTGCGGGAAATTAAGAGCTATCTCGTATCTCA 179
           GACAAGCAAGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTATATACACATCCATTTA
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GACAAGCAAGGCGCTTCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTA
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Best Local
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                                                                                                                                                    The DNA sequence encodes recombinant lipase which has the activity of the known lipase obto. by culturing Geotrichum candidum and is suitable for similar industrial uses e.g. oleic acid esterification as a flavouring agent and in the processing of unsaturated fatty
                                                                                                                                                                                                                  Production of lipase catalysing triglyceride(s) hydrolysis - using recombinant DNA procedures to give DNA segment coding : lipase, cloning vectors and yeast or bacterium transformants
                                                                                                                                                                                                                                                        WPI;
                                                                                                                           Sequence 1831 BP;
                                                                                                                                            acid-contg. oils
                                                                                                                                                                                                 Disclosure; Fig
                                                                                                                                                                                                                                                                         Vandamme E,
                                                                                                                                                                                                                                                                                                             25-APR-1986;
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                                                    TAAAGAAGGACTGAACGGCGGGGGCCACAATACAAATTAA
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                                                                                                                         586 A;
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Pred. No. 8.1
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9.1e-167;
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coeliac disease

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
Nucleic acids encoding lipase in animal feeds, as agents of
                                                                                P-PSDB; AAU83842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus lipase polynucleotide #2
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21-JUN-2001;
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                                                                                                                                                                                                                    (MAXY-) MAXYGEN INC
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enzymes which are useful flavour modification and
as supplements for treating
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                                                                       CAAATTCATGGCGTTGGGCACATTGGTTTATTGATGAACAGCCAAGTCAACAGCCTGATT
                                                                                                                                AGCAGTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAAACGCT
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92.8%;
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1.1e-166;
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RESULT 11
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ABK33827

standard;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease -
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                                                                                                                                                                                                                                                                                                                                            method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 81; Page 120; 196pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giver
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21-JUN-2001;
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                GGCTGGTCACGGGCAAGCTGTATGCGGTTGATTTTTGGGACAAGACAGGGACGAATTAT
                                                                            CACGGTATCGGAGGAGCTTCATACAATTTTGCGGGAATTAAGAGCTATCTCGTATCTCAG
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GGCTGGTCGCGGGACAAGCTGTATGCAGTTGATTTCAAGGACAAGACAGGCACAAATTAT
                                                                                                                       TCGCTGTTTGCGTTGCAACCGTCAGCAAAAGCCCGCTGAACACAATCCAGTCGTTATGGTT
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2001US-300378P
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92.5%;
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Pred. No. 5.2e
0; Mismatches
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RESULT 12
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                                                                                                                                                                                               13-JUL-2000;
21-JUN-2001;
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                                                                                                                                                                                                                                                                                                    Synthetic
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DB; AAU83864.
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2001US-300378P.
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The invention relates to acids encoding them. The

relates to new Bacillus lipase enzymes and the nucleic g them. The lipase polypeptides are useful as supplements as agents of flavour modification and fat modification in

'n in Claim

81; Page 127; 196pp; English

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RESULT 13
ABK33871
ID ABK33
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AC ABK33
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DT 08-MA
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DE Bacil
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KW Lipas
KW Lipas
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Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory
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531; Conser
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Pred. No. 8.2e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding lipase enzymes which are useful in animal feeds, as agents of flavour modification and Crohn's disease and coeliac disease.
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21-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 544 BP; 172 A; 102 C; 138 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giver
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21-JUN-2001;
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                                                                              Sequence 544
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DB; AAU83894.
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21-JUN-2001;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 544 BP; 170 A; 104 C; 140 G; 130 T; 0 other;
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Search completed: May 18, 2003, 06:10:53

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US-09-134-001C-529

US-09-798-096-10

US-08-961-527-258

US-09-007-005-17

US-09-007-005-17

US-09-27-357-149

US-09-134-001C-2256

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US-09-836-329-1

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                 S-08-677-010-1
S-08-790-519-1
S-08-968-563-8
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S-08-232-463-14
S-09-280-116-70
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                   TOPOLOGY:
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Sequence 9, Appli	Sequence 9, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	•	Sequence 65, Appl	Sequence 111, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 1248, Ap	Sequence 1, Appli	Sequence 9, Appli	Sequence 320, App	Sequence 4, Appli	Sequence 5, Appli	Sequence 33, Appl	Sequence 4, Appli

ALIGNMENTS

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Sequence 1, Application US/07930678 Patent No. 5427936
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FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 07
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: EYANS, J.D.
                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MOELLER, Bernhard APPLICANT: VETTER, Roman APPLICANT: WILKE, Detlef APPLICANT: FOULLOIS, Birgit TITLE OF INVENTION: Sequences TITLE OF INVENTION: Lipases
                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1992101:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                          TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
  MOLECULE TYPE:
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                                      STRANDEDNESS:
                                                                                                                                                                                                                   REGISTRATION NUMBER: 26, REFERENCE/DOCKET NUMBER:
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1800 Diagonal Road,
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                                                                              Sequence 14, Patent No. 5
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Best Local Similarity
                                                                  GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
            APPLICANT: SCHEIFL APPLICANT: FALKNER TIȚLE OF INVENTION:
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                                                      APPLICANT: DORNER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKGANISM: Bacillus pumilus DSM STRAIN: DSM 5776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423;
                                                                                 4, Application US/08232463 5670367
SEQUENCES:
                           SCHEIFLINGER, F. FALKNER, F. G.
                         FALKNER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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126..764
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126..221
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222..764
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RECOMBINANT FOWLPOX VIRUS 52
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Pred. No. 7.
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7.8e-89;
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; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 1.3%;
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,766
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
 1081
                                                               1141
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CURRENT APPLICATION DATA
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                      445
                              625 CAAAATACGAA 635
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STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                           265 TTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGT 324
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CITY: Alexandria
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CLASSIFICATION:
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ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
 RRRRRRRRRR 1071
                                                                                           GGTTTATTGATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGGGGGC 624
                                                             AATTACTTATCAAAATTAGACGGTGCTAAAAACGCTCAAATTCATGGCGTTGGGCACATT 564
                                                                                                                                                                                                                     GATCCAAATCAAAAGATTTTATACACATCCATTTACAGCAGTGCCGATATGATTGTCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-978-589A-1
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Best Local
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TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 268
FILING DATE: 26-NOV-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JI., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: trypsin-like serine proteases FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
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                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ESTERASE GENE AND ITS USE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISHII, TO APPLICANT: MITSUDA,
                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337
                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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                                                                                                                                         APPLICATION: NUMBER: US/0: FILING DATE: 26-NOV-1997
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BIRCH, ST
STREET: P.O. BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 CACTTGTAACAATTTTGGTGCTGTCAGTCAGTCGCTGTTTTGCGATGCAGCCGTCAGCAA 88
                                                                                                                                                                                                                                                                                                    COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACCTTGGAATTTCTTTGGCATGTTCTTGAGTACATTGCTGAAGGAGATCTATAAATTT 218
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Pred. No. 0.024;
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                                                                                                                                                                                                                                                                                                                       ; LENGTH: 1089
; TYPE: DNA
; ORGANIZM: E. coli JM 109/paL 612 strain
US-09-336-601-2
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US-09-336-601-2
                                                                           US-09-466-257A-7
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                                GENERAL INFORMATION:
                                            Sequence 7, Application US/09466257A Patent No. 6337190
                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09336601 Patent No. 6184008
                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/336,601
CURRENT FILING DATE: 1999-06-21
EARLIER APPLICATION NUMBER: 09/034,007
EARLIER FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 2
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2185-349P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MITSUDA, Satoshi
TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISHII, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SUGAI, Takeshi
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                                                                                                                                                                                                                                                      Local 5.
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Hwang, Tzann-Shun
Wu, Szu-Pei
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57.8%;
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Pred. No. 0.
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APPLICANT:

Chou, Hsin-Hua Chen, Hwa-Yi Lin, Lung-Shen

APPLICANT:

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                                                                                                                                                                                                                                                                                  ; ORGANISM: Bacillus sphaericus US-09-466-257A-9
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Best Local Similarity
Matches 67; Conserv
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Best Local Similarity 53.6%;
Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chang, Edward
TITLE OF INVENTION: A No. 6337190el D-Amino Acid Aminotransferase For
TITLE OF INVENTION: Simultaneously Producing
TITLE OF INVENTION: Glutaryl-7-Aminocephalosporanic Acid And D-Amino Acid
FILE REFERENCE: 1476-4003
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CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT
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545 TTCAT 549
                                                     648 GTGGAGATATTATCACAGAATGTTCTTCTGCTAATGTCTATGGTATTAAAGATGGTAAAC 707
                                                                          485 GTGCCGATATGATTGTCATGAATTACTTATCAAAATTAGACGGTGCTAAAAACGCTCAAA 544
                                                                                                                            588 GCGCGGTACTTGCGAAACAAGAAGCATCTGAAAAAAGGTTGTTACGAAGCCATTTTACACC 647
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Lin, Lung-Shen
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Wu, Szu-Pei
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                                                                                                                                                                                                                         53.6%;
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Pred. No. 0.8;
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US-08-424-797A-2
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Patent No.
                                                                                               Sequence 2, Application US/08424797A Patent No. 6358714 GENERAL INFORMATION:
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Best Local Similarity
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          APPLICANT: Fothering
APPLICANT: Taylor, P
APPLICANT: Yoshida,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212-758-2982
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA
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                                                                                                                                                                                                                  1001 TTTAT 1005
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
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    Application US/08723896
    5728555

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                                            Yoshida,
                                                              Taylor, Paul P
                                                                              Fotheringham,
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                            Materials and Methods for the
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Production of D-phenylalanine 19
                                             Roberta K.
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Pred. No. 0.87;
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                                                  SEQ ID NO 529
LENGTH: 954
                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        Sequence 529, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
ORGANISM: Staphylococcus epidermidis - 09-134-001C-529
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964
                                                                                                     PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                    NUMBER OF SEQ ID NOS:
                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    1001 TTTAT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Thomas C. REGISTRATION NUMBER: 36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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EDNESS: single
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cker Drive, 6300 Sears Tower
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US-08-961-527-258
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                                                                                                                                                                                                                                                Sequence 258, Application US/08961527 Patent No. 6420135
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Matches
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CURRENT FILING DATE: 2001-03-01
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APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                  21854 AACCACCAAGAACAGAATCATGAAGAAAACAGAAAATCTGAACAGACCTATAACTAGTAAGG 21913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                STREET: 9410
CITY: Rockville
CTATE: Maryland
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                                                  NUMBER OF SEQUENCES:
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nes 103; Cónserv
                 COMPUTER:
                                                                                                                                                  ADDRESSEE:
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                                                                                                                               E: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                                                                                                                                                              Charles Kunsch
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               E: Diskette, 3.5
HP Vectra 486/33
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 MSDOS
                                                                                                                                                                                              Streptococcus pneumoniae
                                3.50 inch, 1.4Mb storage
version 6.2
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Pred. No. 0.96;
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SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US

US/08/961,527

PRIOR APPLICATION DATA:

CLASSIFICATION:

DATE:

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US-08-441-139-8
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Best Local Similarity 48.8%;
Matches 83; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 15-MAY-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1431
                                        FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1371 GGAACGAGTTTTGAACAAGTAGATAGGGTTGTTTCCGAAAATCCAGCAGATACTTTACTT 1430
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                  COUNTRY: UZIP: 11530
                                                                                                                                                                                                                                                                                                             STREET:
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REFERENCE/DOCKET
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                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                      Wittrup, Dr. Karl D.
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                                                                                                                                                                                                                                                                                                                           SCULLY,
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                NUMBER:
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                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27 EARLIER APPLICATION NUMBER: 60/064,491 EARLIER FILING DATE: 1997-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003
                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ
                                                                                                                                                PEATURE:
NAME/EVE: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                   LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION:
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LENGTH: 6030 base pair
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TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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                             264 ATTTGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAG 323
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                                                                 Local Similarity
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Local Similarity 51.48;
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CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EEARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
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US-09-244-796-17
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Best Local Similarity 2.6%;
Matches 5; Conservative 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
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US-09-991-936-476	US-10-067-514-1	US-09-764-891-8240	US-09-938-842A-1436	US-10-123-155-412	US-08-781-986A-127	US-09-864-761-8107	US-08-781-986A-3578	US-09-783-590-8898	US-10-105-877-4	US-09-811-469-3	US-09-983-802-149	US-10-026-188-3	US-09-764-847-1876	US-10-092-154-1876	US-10-123-155-10	US-09-991-936-1676	US-09-867-701-1711	US-09-954-531-382	US-09-912-020-221	US-09-770-445-100	US-09-918-995-36871	US-09-938-842A-3864	US-09-878-766A-19	US-09-878-781-11	US-09-770-149-76
Sequence 476, App		Sequence 8240, Ap		Sequence 412, App	Sequence 127, App		Sequence 3578, Ap	Sequence 8898, Ap	Sequence 4, Appli	Sequence 3, Appli	Sequence 149, App	Sequence 3, Appli	Sequence 1876, Ap	Sequence 1876, Ap	Sequence 10, Appl	Sequence 1676, Ap	Sequence 1711, Ap	Sequence 382, App		Sequence 100, App	Sequence 36871, A			Sequence 11, Appl	Sequence 76, Appl

ALIGNMENTS

RESULT 1 US-10-028-247-3

GENERAL INFORMATION:

APPLICANT: Goldman, Stanley

APPLICANT:

Sequence 3, Application US/10028247 Patent No. US20020150594A1

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                                                                                                                                                                                                        ; NAME/KEY: CDS
; LCCATION: (1)...(639)
; OTHER INFORMATION: lipase 396
US-10-028-247-3
                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 3
LENGTH: 639
TYPE: DNA
                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                      Matches 631;
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 00/214.164.
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/028,247
CURRENT FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Methods and Compositions for Developing Spore Display TITLE OF INVENTION: Systems for Medicinal and Industrial Applications FILE REFERENCE: 18097A-033520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                               ORGANISM: Bacillus circulans
                                                                                                                                                                                                                                                                               FEATURE:
61
                                61
                                                                                     TCGCTGTTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT 120
TCGCTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTT
                                                                   Maxygen, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lathrop, Stephanie J
Longchamp, Pascal F.
Whalen, Robert G.
                                                                                                                                      Conservative
                                                                                                                                                       98.0%;
98.7%;
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                                                                                                                                                     Score 626.2; DB 12
Pred. No. 9.3e-187;
                                                                                                                                      Mismatches
                                                                                                                                                                12; Length 639;
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                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)..(1011)
US-09-878-781-9
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CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 9
LENGTH: 1011
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09878781
Publication No. US20030082781A1
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: POtter, Andrew A. TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GapC PROTEIN AGAINST TITLE OF INVENTION: STREPTOCOCCUS INFECTION FILE REFERENCE: 9000-0055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bolton, Alexandra J. APPLICANT: Perez-Casal, Jose
                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Streptococcus parauberis
                                                                                                                                                                                                                                                              FEATURE:
327 GGGTGGCGCGAACACCACCATACTACATAAAAAATCTGGACGGCGGAAATAAAATTGAAAA 386
                                                       315 TGCTGAAAAACATTTACATGAAAAATGGTGCTAAAAAAGTTGTTATCACTGCTCCTGGTGG 374
                                                                        267 TGTGCAAAAGGTTTTAGACGAAACGGGTGCGAAAAAAGTGGATATTGTCGCTCACAGTAT 326
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                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perez-Casal, Jose
Fontaine, Michael
                                                                                                                                  Conservative
                                                                                                                                                   56.9%;
                                                                                                                                  0;
                                                                                                                                                 Score 38.2; DB 9; Pred. No. 0.13;
                                                                                                                                  Mismatches
                                                                                                                              53;
                                                                                                                                                                  Length 1011;
                                                                                                                                Indels
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RESULT 4
US-08-781-986A-4008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC TITLE OF INVENTION: AGAINST STREPTOCOCCUS INFECTION FILE REFERENCE: 9000-0057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Potter, Andrew A. APPLICANT: Perez-Casal, Jos APPLICANT: Fontaine, Michae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Streptococcus parauberis FEATURE:
                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 AGT 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 TGCTGAAAAACATTTACATGAAAAATGGTGCTAAAAAAGTTGTTATCACTGCTCCTGGTGG 374
                                                                                           COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
SOFTWARE: ASCII Text
                                       APPLICATION NUMBER: US/08/781,986A FILING DATE:
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                   STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGATGACGTGAAAACAGTTGTATTTAACACTAACCATGATATCCTTGATGGAACTGAAAC
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70; Conserv
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Pred. No. 0.13;
0; Mismatches 53;
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ATTORNEY/AGENT INFORMATION:

Benson,

APPLICATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.9%;
Best Local Similarity 53.8%;
Matches 77; Conservative
                                                              ATTOKNEL/...

NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB24/
TELECOMMUNICATION INFORMATION:
THE TEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                 NEORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                      507 TTACTTATCAAAATTAGACGGTGCTAAAAAACGCTCAAATTCATGGCGTTGGGCACATTGG 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         567 TTTATTGATGAACAGCCAAGTCA 589
                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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               ENGTH:
                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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: 13321 base pairs nucleic acid
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RESULT 7 US-09-938-842A-3605/c

Sequence 3605, Application Patent No. US20020160378A1 GENERAL INFORMATION:

APPLICANT: Harper, Jeff

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Best Local Similarity
Watches 77; Conserv:
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US-09-991-936-852/c
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                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/128,704
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US/09/543,668 PRIOR FILING DATE: 2000-04-07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF FILE REFERENCE: FC-6-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/991,936
CURRENT FILING DATE: 2001-11-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brandt, Kevin S.
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321 CAA 319
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                                                                                                                                                                                                                                                                                 Local Similarity 49.7 les 91; Conservative
                                                                    AATAAAAATGCCAGTAAATAGTAAACTTAATAATAATTTTATTGACAAATATCAAAATTC
                                                                                                      GATGAACAGCCAAGTCAACAGCCTGATTAAAGAAGGACTGAACGGCGGGGGGCCAAAATAC
                                                                                                                                      TGCACAACAATATTTTGCTAAAATCGTTTTAATTTACATGTCTGCATAAAAJAATAACTT
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Stinchcomb, Dan T.
Wisnewski, Nancy
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Pred. No. 1;
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
EQ ID NO 3605
LENGTH: 785
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APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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Patrick J. Dillon
                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
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                                                                                                                                                                                                  APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Maryland
                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc
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Pred. No. 1.6;
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                                                                                                                                                                                                                                                                                 SEQ ID NO 412
LENGTH: 546
TYPE: PRT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Publication No.
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-66-28
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C227
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CGCTCACAGTATGGGTGGCGCGAACACACCTTACTACATAAAAAATCTGGACGGCGGAAA 374
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Pred. No. 2.3;
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CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 612
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
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                                                                                               TCCGGGAACAGATCCAAATCAAAAGATTTTATACACATCCATTTACAGCAGTGCCGATAT 494
                                                                                                                                                                  CGGCGGGGGCCAAA 628
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.MH.TNMA.Y.Y.MH.AW.NN.N..Y.MN.SB.S..BT.
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96; Mismatches
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Sequence 1, Application US/10147467 Publication No. US20030027295A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
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                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Genbank Accession No. US20020119462A1 AI169239
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                                                                                                                                                                      303 AGTGGATATTGTCGCTCACAGTATGGGTGGCGCGAACACCACCTTACTACA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/298,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/297,457
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Elashoff, Michael
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56.4%;
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Pred. No. 3
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Mismatches
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APPLICANT: TAKESHI, IShii APPLICANT: SATOSHI, Mits

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RESULT 14
US-09-731-872-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 536165
; TYPE: DNA
; ORGANISM: Rhizobium
US-09-939-964-1
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US-09-939-964-1
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; TYPE: DNA
; ORGANIZSM: Burkholderia cepacia
US-10-147-467-1
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 88; Conserv
                                                    GENERAL INFORMATION
                                                                      Sequence 18, Application US/09731872 Patent No. US20020102604A1
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Best Local
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CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 4
APPLICANT:
                              APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genomic Sequence
TITLE OF INVENTION: Plasmid
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                                                                                                                                                                                                                                                                                                        115 ATGGTTCACGGTATCGGAGGAGCTTCATACAATTTTGCGGGGAATTAAGAGCTATCTCGTA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 TGGCCCGGTATTATCACGATTTGTGCAAAAGGTTTTTAGACGAAACGGGTGCGAAAAAAGT 305
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                                                                                                                                                                                                                                                                   ATCTTAGAGATGCTCGAAGAAGATATAAAGGATCTAGAGGGAGCGAGGCGAGAGCGCGTA 223336
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                Bougueleret,
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Broughton, William John
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Sequence 1896, Application
Patent No. US20020146721A1
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                                                                                                                                                                                                                      US-09-974-300-1896
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Best Local S
Matches 62
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                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods For Monitoring Multiple TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
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                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/279,526
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gi
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                                                                                                                                                                                                                                   LENGTH: 432
TYPE: DNA
ORGANISM: Bacillus licheniformis
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 94..210
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NAME/KEY: CDS
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70
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                                                                                                                                                            Local
                                                                                                     CTGTTTGCGATGCAGCCGTCAGCAAAAGCCGCTGAACACAATCCAGTTGTTATGGTTCAC 123
                                                                    AAACTTCTAGGAATTATGATGACGATTATTTTGGCAATTGCTGTGTTGGGAACCGCTGCG
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Pred. No. 6.4;
0; Mismatches
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Pred. No. 11;
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length: 2000000000
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Match Length DB
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ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 CNSOOL78 LOCUS ACCESSION VERSION KEYWORDS COMMENT SOURCE ORGANISM DEFINITION JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101) CNS00L78 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR24B18 of RPCI-98 library from Drosophila melanogaster (fruit please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, GSS. riy), genomic survey sequence. AL068157 Genoscope. Direct Submission AL068157.1 The library is named RPCI-98 and was constructed GI:4958085 in by

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                               126 Natural Resources, East Lansing,
Tel: 517 353 4751
                                                                                                                                                                                                                                                     Michigan State University
                                                                                                                                                                                                                                                                       Department of Forestry
                                                                                                                                                                                                                                                                                           Contact: Kyung-Hwan Han
                                                                                                                                                                                                                                                                                                             black locust (Robinia pseudoacacia) Unpublished (2002)
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                                   /organism="Robinia pseudoacacia"
/db_xref="taxon:35938"
/clone_lib="SWS (Sapwood of black locust -/cissue_type="sapwood"
/dev_stage="mature tree"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At2g19740. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line
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Li,Y., Strizhov,N.,
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H and Weisshaar,B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                       ø
                       removed"
                                                                                                                                                      /clone="GK-203F11-014507"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         black locust tree collected in Michigan in late July." a 124 c 101 g 228 t 5 others
                                                                were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          /strain="Columbia
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                       С
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosso, M. and Weisshaar, B.
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(GABI-Kat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTCATTTAAAGATAA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATGATAAATGACCAAAATAGGTAAGTGATCAAAACAAGCAAAGTCTTTTCGTTTAGTA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Jeffery L. Miller
Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
National Institute of Diabetes and Digestive and Kidney Diseases
Deciding 10, Room 9B17, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 354)
Gubin, A.N., Njoroge, J.M., Bouffard, G.G. and Miller, J.L.
Gene expression in proliferating human erythroid cells
Genomics 59 (2), 168-177 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intramural Sequencing Center (NISC).

Plate: 03 row: b column: 04

Seq primer: -40M13 forward primer (Amersham).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 402 2373
Fax: 301 435 5148
Email: jm/fenih.gov
DNA Sequencing and analyses by National Institutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                        (Clontech) according to the manufacturer's protocol and cloned into EcoRI digested Lambda 2ap II vector
                                                                                          cytometric separation after a 5-day culture period in the presence of erythropoietin. Total RNA was purified from the sorted cell population using TRIzol reagent. RNA (0.3 ug) was converted into double stranded cDNA using Clontech's CapFinder cDNA Library Construction Kit
                                                                                                                                                                                        /note="Organ: blood; Vector: Lambda ZAP II; Site_1: EcoRI;
Site_2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
                                                                                                                                                                                                                                            /cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax03b04"
/clone_lib="Proliferating
                     to in vivo excision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                       (Stratagene). The phage library was
                                                                                                                                                                                                                                                                                                                         /tissue_type="blood"
/cell_type="Erythroid Cells"
                                                                                                                                                                                                                                                                                                                                                                /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                   Erythroid Cells (LCB:ax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T., Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                            Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ989712 646 bp DNA linear GSS: Rfc00339 Photorhabdus luminescens strain W14 M13 library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biology and University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: ffrench-Constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus luminescens
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                                                                                                                                                                                                                                                                                                       Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                 h Building, Bath BA2 7AY,
(44) 1225 826621
(44) 1225 826779
                                                                                                                                                                                                                                                                                                                                          K12 genome) please
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        throughput (NIH intramural sequencing center http://www.nisc.nih.gov/)."
a 66 c 78 g 123 t
                                                                            kb)
                                                                                                                                                                      /strain="W14"
/db_xref="taxon:29488"
/clone="PLG00339"
                                                        /note="Genomic DNA from strain W14 was size kb) and then cloned into M13 Janus."  
118 c  
185 g  
165 t  
15 others
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                     library
                                                                                                                                                                                                                           /organism="Photorhabdus
                                                                                                               /dev_stage="primary phase variant"
                                                                                                                                                    /clone_lib="Photorhabdus luminescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 to 646)
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 Score 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following repetitive elements were found in this cDNA sequence: 1-36, >AT_rich#Low_complexity (matched compliment) 280-325, >(TA)n#Simple_repeat (matched compliment) 636-702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index 
Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
ייביוריים רפייסיי Tnstitute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
1 (bases 1 to 704)
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58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (matched compliment)
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                                                                                                                                                                                                                                                 to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
                                                                                                                                                                                                                                                                                                                                                                          library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned to an EcoR I adaptor, digested with Not I, and cloned
                                                              TAG_SEQ-AGAATCCGGC"
                                                                                                                                                                                       library is AGAATCCGGC. The ce
James Martin from University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B (Life Technologies)"
/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR ; Site_2: Not I; NCI_CGAP_FHO is a cDNA library containing the following tissue(s): Human Grade 1 Chondrosarcoma Cell Line The
                                                                                                                            TAG_TISSUE=Human Chondrosarcoma
                                                                                                                                                            TAG_LIB=UI-H-FHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UI-H-FHO-bci-l-19-0-UI"
/clone_lib="NCI_CGAP_FHO"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Human Chondrosarcoma Cell Line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bento Soares, bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:21983653
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Bento Soares, University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further is
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., (A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., N., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Y., Person,B., Swaller,T., Gibbons,M., Pape,D., R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Ca,R., Waterston,R., and Wilson,R.
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Washington University School of Medicine
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EST.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                     www.resgen.com
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                      XhoI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings
                                                                                                                                        /tissue_type="whole seedlings
/dev_stage="1 week old"
/lab_host="DH10B"
                                                                                                                                                                                                             /clone="SOYBEAN CLONE ID:
/clone_lib="Gm-c1052"
                                                                                                                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                  /note="Vector: pBluescript II SK+; Site_1: EcoRI;
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                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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/tissue_type="Hypocoty1, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
/note-"Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2:
/note-"This cDNA library was constructed from mRNA isolated
from etiolated hypocoty1 tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
                                                                                                                                                 /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1045-1141"
/clone_lib="Gm-c1045"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,A., Bolla,B., Marra,M., Hiller,L., Kucaba,T., Martin,J., E Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., E Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., P Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                             Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4563 or contact via email: ccu@resgen.com
High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG043888 444 bp mRNA linear EST 28-NOV-2001 saa34d09.yl Gm-c1059 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1059-930 5', mRNA sequence.
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Contact: Shoemaker R/Public Soybean EST Project
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Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Public Soybean EST Project
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from 2 week old etiolated whole seedlings of PI468916. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI XhoI
                                                                                                         /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
                                                                                                                                                                                                              /clone="GENOME SYSTEMS CLONE ID: Gm-c1059-930"
/clone_lib="Gm-c1059"
                                                                                                                                                                                                                                                                /organism="Glycine max"
/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                         /tissue_type="Whole seedling, 2 week old, etiolated"
/lab_host="DH10B"
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69.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
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South Memorial Parkway Huntsville, AL 35801 For furt
call: (800)-533-4363 or contact: ccu@resgen.com web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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synthesized from mRNA using a primer consisting of a poly(dT) primer with a XhoI restriction site: EcoRI adapters were ligated to the blunt-ended cDNA fragmu
                                                                                                                          note="Vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: XhOI; This cDNA library was constructed from mRNA isolatifrom etiolated hypocotyl tissue of 9-10 day old seedling of the cultivar Williams 82. Complementary DNA was
                                                                                                                                                                                                                                                                                                 /tissue_type="Hypocotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
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/clone_lib="Gm-c1045"
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/db_xref="taxon:3847"
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Pred. No. 3.9;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J.; I Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., N., R., Materston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available through: ResGen, Inv
South Memorial Parkway Huntsville, AL 35801
call: (800)-533-4363 or contact: ccu@resgen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Shoemaker R/Public Soybean EST Project
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h quality sequence stop: 426.
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314 286 1810
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Phytophthora soyae race 1 and tissues were harvested 2 and 4 hours following infection. The library is the pool of these two time points. Complementary DNA was synthesized
                                                                /note="Vector: pBluescript II SK+; Site_1: EcoRI; XhoI; The cDNA library was contructed by M. Bhatta from mRNA isolated from etiolated hypocotyls from cultivar Williams 82. Tissue was inoculated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restriction site of the \, pBluescript vector. The ligated cDNA fragments were transformed into DH10B \, host cells
                                                                                                                                                      /tissue_type="Etiolated hypocotyls
/lab_host="DH10B"
                                                                                                                                                                                               /clone="SOYBEAN CLONE ID: Gm-c1084-3626"
/clone_lib="Gm-c1084"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                  /db_xref="taxon:3847"
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69.4%;
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301 For further i
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CLONE ID:
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                                                                                                                                     Site_2:
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanns, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 9-10 day old etiolated
                                                                       /clone="SOYBEAN CLONE ID: Gm-c1069-5289"
/clone_lib="Gm-c1069"
/tissue_type="Degenerating cotyledons, 9
etiolated seedling"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BM954950 539 bp. sam75c01.yl Gm-c1069 Glycine max Gm-c1069-5113 5', mRNA sequence:
                                                                                                                                                                                                                                                                                                                       Email: estéwatson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                soybean.
Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoemaker,R., Keim,P., Vo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Fabaceae; Papillonoldeae; Phaseoleae;
                                                                                                                                                                                                                                                                                                 www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project
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                                           etiolated seedling"
/lab_host="DH10B"
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
                                                                                                              /clone="SOYBEAN CLONE ID: Gm-c1069-5113"
/clone_lib="Gm-c1069"
                                                                                                                                                            /organism="Glycine max"
/db_xref="taxon:3847"
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                                                                                           /tissue_type="Degenerating cotyledons, 9-10 day old
                                                                                                                                                                                                                             location/Qualifiers
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69.4%;
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    Hillier,L., Kucaba,T., Martin,J.,
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SOURCE KEYWORDS VERSION

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A genomic sample sequence of the entomopathogenic bacterium
                                                                                                                                                                                                                                                                                                                                  annotation of identified clones (BLASTA, pundantoration of identified clones (BLASTA, pundantoration of identified clones (BLASTA)
                                                                                                                                                                                                                                                                                                                                         This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Biology and Biochemistry University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ991444 661 bp DNA linear Rfc02380 Photorhabdus luminescens strain W14 M13 !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: ffrench-Constant RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (44) 1225 826621
(44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                              bssrfc@bath.ac.uk
    Ω
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                         kb)
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library was constructed in the
/dev_stage="primary phase variant"
/note="genomic DNA from strain W14 was size selected
kb) and then cloned into M13 Janus "
194 c 124 g 167 t 6 others
                                                                                               library
                                                                                                                   /clone_lib="Photorhabdus luminescens strain W14
                                                                                                                                                                                                            /organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                           /clone="PLG02380"
                                                                                                                                                             /db_xref="taxon:29488"
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coratory of Dr. Randy
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Matches 110; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.
Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,K.,
Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R.,
Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ458251 676 bp mRNA linear EST 30-MAY-200 ko58b05.yl Toxoccara canis adult SL1 TOPO vl Toxoccara canis cDNA similar to TR:076556 076556 C09E8.2 PROTEIN. [1] ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at Washington University, St. Louis. Adult nematodes were collefrom infected dogs and provided by Dr. Prema Arasu of North Carolina State University, Raleigh, NC (Prema_Arasuencsu.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Washington Univ. Nematode EST Project, 1999 Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing by: Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The library was constructed by Claire Murphy and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxocara canis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toxocaridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: SL1 primer
                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 525
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allen, M., Person, B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       est@watson.wustl.edu
                                                                          were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Adult nematodes were collected from infected dogs and provided by Dr. Prema Arasu of North Carolina State University, Raleigh,
                                                                                                                                                                                   can's cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end
                                                                                                                                                                                                                                      Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Adult Toxocara
                                                                                                                                                                                                                                                                                   /note="Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI;
Site_2: EcoRI; The library was constructed by Claire
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Toxocara canis adult SL1 TOPO v1"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Toxocara canis"
/db_xref="taxon:6265"
                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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                          (Prema_Arasu@ncsu.edu)."
143 c 179 g 167 t
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60.8%;
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Pred. No. 6.9;
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                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Louis. Adult nematodes were collected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
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